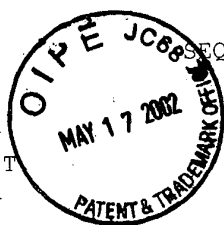


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SEQUENCE LISTING

<110> Cali, Brian M.
Holtzman, Doug
Madden, Kevin T
Milna, G. Todd
Sherman, Amir
Silva, Jeffry C.
Trueheart, Josh
Zhang, Lixin

<120> Novel Regulators of Fungal Gene Expression

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<141> 2001-12-22

<150> US 60/257,431

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<220>

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<210> 2
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 <213> Artificial Sequence

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			20					25					30		
Ala	Asn	His	Phe	Lys	Leu	Lys	Leu	Arg	Thr	Asp	Asp	Pro	Asn	Ser	Val
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Lys	Leu	Leu	Glu	Arg	Tyr	Asp	Gln	Trp	Phe	Asp	Asn	Gly	Phe	Ala	
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Lys	Leu	Leu	Ser	Ala	Arg	Met	Ala	Ser	Lys	Glu	Ser	Arg	Lys	Lys	Arg
65					70					75					80
Lys	Asp	Glu	Ala	Ser	Thr	Ser	Asn	Thr	Thr	Lys	Arg	Thr	Arg	Ser	Gln
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Leu	Arg	Leu	Leu	Arg	Ser	Ser	Asn	Gly	Thr	Lys	Ser	Asn	Val	Leu	Pro
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225					230					235					240
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Pro	Ile	Pro	Lys	Gly	Gly	Leu	Thr	Arg	Thr	Arg	Ser	Thr	Arg	Leu	Thr

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Pro	Arg	Gly	Gly	Phe	Asp	Val	Phe	Val	Asp	Glu	Arg	Lys	Glu	Glu	Glu		
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Asp	Ser	Lys	Thr	Thr	Tyr	Gln	Gln	Pro	Gly	Phe	Arg	Ala	Gln	Phe	Asp		
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Thr	Leu	Thr	Pro	Thr	Arg	Leu	Val	Leu	Asn	Gly	Lys	Thr	Asn	Ala	Gly		
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Ile	His	Ala	Pro	Arg	Ile	Gly	His	Ala	Ser	Leu	Ala	Lys	Glu	Asn	Ile		
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Glu	Pro	Ile	Leu	Asn	Pro	Gln	Gly	Arg	Ile	Ala	Pro	His	Gly	Trp	Asn		
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Ser	Pro	Phe	Val	Lys	Tyr	Pro	Asp	Ser	Asp	Asp	Phe	Gly	Phe	Gly	Pro		
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Ser	Tyr	Leu	Pro	Asp	Leu	Gly	Asp	Thr	Tyr	Asp	Thr	Leu	Asp	Lys	Ala		
			500					505					510				
Gly	Tyr	Arg	Ser	Asn	Pro	Leu	Gln	Ala	Pro	Ser	Lys	His	Pro	Phe	Tyr		
	515						520					525					
Glu	Ser	Gln	Tyr	Glu	Glu	Glu	His	Thr	Ala	Ala	Gln	Asn	Gly	Trp	Leu		
	530					535					540						
Pro	Val	Asp	Gln	Ile	Val	Pro	Ser	Asp	Val	Thr	Ile	Pro	Glu	Asp	Asp		
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<212> DNA
<213> Artificial Sequence
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<220>
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939

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

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 Pro Pro Leu Asp Arg Tyr Tyr Ala Ile Lys Val Phe Arg Arg Ser Pro
 35 40 45
 Gly Gln Ser Thr Asp Glu Tyr Thr Lys Gln Val Asn Ala Glu Phe Ala
 50 55 60
 Val Val Ala Asn Leu His His Gln His Val Val Ser Thr Phe Glu Leu
 65 70 75 80
 Leu Pro Ile Gly Gly Gly Asn Leu Ala Ala Cys Met Glu Tyr Cys Ala
 85 90 95
 Gly Gly Asp Leu His Ser Leu Ile Thr Ala Gly Pro Ser His Arg Leu
 100 105 110
 Pro Ser Glu Glu Ala Asp Cys Leu Phe Lys Gln Leu Leu Arg Gly Ile
 115 120 125
 Ser Tyr Leu His Lys Ser Gly Ile Ala His Arg Asp Leu Lys Pro Glu
 130 135 140
 Asn Leu Leu Leu Thr His Arg Ala Cys Leu Lys Ile Ser Asp Phe Ala
 145 150 155 160
 Asn Ala Glu Arg Val Arg Phe Asp Gly Asp Asp Ser Gln His Ala Asn
 165 170 175
 Asp Leu Ala Glu Thr Glu Arg Arg Ser Leu Glu Pro Thr Pro Tyr Leu
 180 185 190
 Ala Pro Glu Arg Tyr Leu Asp Glu Gly Asp Arg Tyr Met Ser Arg Ser
 195 200 205
 Asp Pro Arg Ala Leu Asp Ile Trp Ala Ala Ala Val Ile Tyr Val Ala
 210 215 220
 Met Arg Thr Gly Arg Asn Leu Trp Lys Ala Ala Thr Glu Lys Asp Glu
 225 230 235 240
 Gly Phe Arg Ala Tyr Val Glu Glu Arg Lys Ala Glu Lys Thr Asn Thr
 245 250 255
 Val Ile Gln Asp Ser Cys His Glu Arg Gly Arg Lys Val Ile Tyr Ala
 260 265 270
 Met Leu Ser Thr Asp Pro Gly Lys Arg Pro Ile Ala Thr Glu Ile Leu
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<210> 5
 <211> 1512
 <212> DNA
 <213> Artificial Sequence

<220>

<223> fungal gene

<400> 5

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<210> 6

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 6

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Ser Ile Pro Glu Ser Met Arg Gln Tyr Leu Ala Met Gln Phe Asp Pro
35     40     45
Ser Lys Pro Gly Ala Arg Asp Pro Phe Gly Arg Thr Gly Gly Tyr Gly
50     55     60
Ala Asn Gly Ala Tyr Pro Asn Glu Pro Thr Pro Ser Gly Lys Val Val
65     70     75     80
Ile His His Phe Thr Cys Arg Ser Leu Thr Ile Gly Ser Trp Arg Arg
85     90     95
Ile Gly Gln Asn Ala Met Asp Leu Val Val Phe Tyr Ser Pro Glu Lys
100    105    110
Ala Cys Met Thr Tyr Tyr Ile Asn Asn Asp Ala Ala Gly Tyr Lys Ile
115    120    125

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Glu Tyr Pro Phe Ser Tyr Ile Lys Asn Ile Thr Leu Glu Ser Gly Asp
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Gln Gly Pro Gln Pro Asn Gly Ala Pro Pro Arg Pro Thr Gly Leu Val
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Val Glu Leu Asn Arg Pro Pro Leu Phe Tyr Met Asp Ser Ser Asn Ser
          165          170          175
Gly Gly Phe Tyr Gln Cys Gly Asp Phe Thr Glu Asp Gln Gln Ala Ser
          180          185          190
Ser Val Met Ile His Arg Leu Gly Gly His Pro Lys Val Leu Ser Val
          195          200          205
Gln Leu Ala Lys Leu Val Ser Leu Glu Ser Phe Gln Asn Arg Leu Ala
 210          215          220
Tyr Gly Asn Phe Pro Ala Asn Asn Ser Met Ser Pro Pro Phe Ile Gln
 225          230          235          240
Arg Pro Ala Ser Gln Pro Asn Gln Phe Ala Pro Ala Phe Met Ser Met
          245          250          255
Tyr Ala Glu Asn Pro Ala Val Met Asn Leu Gln Ala Ala Arg Gly His
          260          265          270
Lys Arg Gln Arg Ser Arg Ser Val Pro Val Ala Ile Asp Phe Ser Ala
          275          280          285
Leu Gly Ala Pro Met Thr Gln Phe Ser Met Pro Gln Ala Gln Gln Phe
 290          295          300
Ser Gln Ala Asp Ser Gly Ile Tyr Ala Pro Ile Pro Gln Ser Thr His
 305          310          315          320
Ser Leu Ala Ala Asn Leu Arg Ile Asp Thr Ser Ser Gly Tyr Ala Phe
          325          330          335
Asp Pro Arg Ala His Pro Met Ser Ala Thr Thr Thr Ala Ser Pro Ser
          340          345          350
Asp Phe Ala Ser Pro Ala Leu Phe Ser Ala Gly Pro Gln Gly Asp Ser
          355          360          365
Thr Pro Val Gly Ser Val Gly Ala Gln Phe Thr Leu Pro Tyr Val Ser
 370          375          380
Pro Ala Val Asp Ser Gly Val Ser Thr Gln Ala Ala Ser Pro Tyr Ser
 385          390          395          400
Asn Val Ser His Val Asp Pro Met Ile Ala Asn His Ser Pro Pro Leu
          405          410          415
Thr Asn Met Ser His Thr Pro His Asp Val Tyr Gly Met Gly Ser Glu
          420          425          430
His Gln Pro Ser Tyr Thr Glu Glu Gly Met Pro Met Gly Gly Gly Met
          435          440          445
Tyr Lys His Ile Asn Phe Ser Ser Val Pro Thr Thr Val Gly Leu Glu
 450          455          460
Gly Asn Ala Phe Asp Leu Pro Met His Ser Met Ser Gly His Ala Ser
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Pro Gly Val Gln Gly Asp Tyr Gln Gly Ile Ala Leu Glu Asn Val Asp
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Pro Asn Val Leu Thr Pro Gly Ser
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<210> 7

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 7

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gcggtacacc agactatggg cttcccaatg tcatccgtca acgggatggg ccgtgggtcag 1140
cctgaagacg cgtttcccg gcggccggcc catcaaggag ccccttggcc acaagctccc 1200
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<210> 8

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 8

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20          25          30
Pro Gln Tyr Thr Met Gln Pro Gln Tyr Pro Val Ser Gln Pro His Thr
35          40          45
Leu Pro Pro Leu Gln Pro His His Ser Gln Ser Pro Ala Pro His Ser
50          55          60
Tyr Met Gly Gln Pro Pro Tyr Arg Pro Asp Leu Asn Arg Tyr Pro Ala
65          70          75          80
Ser Ser His Asp Val Tyr Ala Ser Ser Ala Ala Pro Ile Met Pro His
85          90          95
Thr Thr Val Gly Ser Leu Pro Pro Thr Ser Phe Leu Ser His Pro Asn
100         105         110
Pro Gln Ala Gln Ala Gln Ala Gln Gln Ser Pro His Tyr Pro Pro Pro
115         120         125
His Ser Val Leu Pro Pro Ala Ser Ser Ala Gln Ser Tyr Pro Gln Pro
130         135         140
Ile Ala Pro Ala Pro Pro Arg Asp Arg Arg Ala Asp Phe Asn Asn Gly

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145          150          155          160
Leu Pro Ser Gly Ala Phe Ser Tyr Ser Asp Gly Lys Pro Gln Gly Trp
          165          170          175
Asp Pro Val Ala Ala Asn Gly Ala Ala Pro Tyr Pro Gly Lys Asp Ser
          180          185          190
Pro Arg Thr Gln Val Val Gly Ser Gln Gly Arg Arg Gly Ile Leu Pro
          195          200          205
Ser Val Pro Gly Arg Ala Thr Pro Val Thr Asn Gly Val Asn Gly Thr
          210          215          220
Gly Lys Asn Thr Thr Ile Pro Ala Lys Asp Ala Asp Gly Lys Phe Pro
225          230          235          240
Cys Pro Asn Cys Asn Lys Thr Tyr Leu His Ala Lys His Leu Lys Arg
          245          250          255
His Leu Leu Arg His Thr Gly Asp Arg Pro Tyr Met Cys Val Leu Cys
          260          265          270
Lys Asp Thr Phe Ser Arg Ser Asp Ile Leu Lys Arg His Phe Gln Lys
          275          280          285
Cys Ser Ile Arg Arg Gly Asn Pro Thr Gly Ala Thr His Leu Ser His
          290          295          300
Pro Asn Ala His Val Lys Arg Ser Gln Gln Gln Ala Ala Ala Asn Pro
305          310          315          320
Val Lys Pro Val Gln Asp Glu Val Ser Ser Thr Val Pro Pro Pro Asn
          325          330          335
Gly Ile Pro Gly Thr Thr Tyr Gly Glu Gly Ala Val Asn Gly Asn Gly
          340          345          350
Leu Ala Pro Ala Arg Pro Gly Tyr Ala Asp His Gln Thr Met Gly Phe
          355          360          365
Pro Met Ser Ser Val Asn Gly Met Gly Arg Gly Gln Pro Glu Asp Ala
          370          375          380
Phe Pro Gly Gly Arg Pro His Gln Gly Ala Pro Trp Pro Gln Ala Pro
385          390          395          400
Lys Gln Ser Pro Tyr Leu Val Gln Pro Gly Ala Asp Pro Ser Gly His
          405          410          415
Gln Leu Asn Ile Asp Arg Asn Ile Glu Gln Val Lys Gln Pro Val Val
          420          425          430
Gln Asp Pro Lys Arg Pro Val Met Pro Gly His Pro Gly His Pro Gly
          435          440          445
Glu Leu Asp Trp Thr Ser Met Phe Gln Pro Gln Ala Pro Glu Gly Tyr
          450          455          460
Met Phe Ser Gln Ser Met Pro Gly Gly Gln Glu Pro Ile His Ala His
465          470          475          480
Val Glu Thr Glu Arg Lys Tyr Tyr Pro Thr Thr Thr Ala Gly Gln Glu
          485          490          495
Ser Gly Met Asn Gly Leu Tyr Leu Ala Ser Thr Met Ser Gly Asp Gly
          500          505          510
Thr Val Gln Pro Ala Arg Gln
          515

```

<210> 9

<211> 1116

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 9

```

atgattaatg agacgcagga gattcaactcc gagaacgaca tcgacagagc gccgatgcga 60
tcgtcgattg agctgccttc tctccgtgat cacttcaaac gggactcggt gcctccattt 120
tcgtcccctc aacctagatc gctcctaccc tcgattctca accactctcc tcccggtcgc 180
tcttcgaccc ttccgccgat ccagcggacg aacaagcttc cccgacctcg caaaggatcg 240
ataaccgggg cgcgaaaagc caagcatgaa cggtcgaggt cgaaaagatt tggtaggcgc 300
ccgagcatag gcgataggaa ggctctatca gcagaaccgc aaaccgctgc ctggggcgag 360
ggcaagcggt gggaggatct cattgaggcg gccacatcag caaccgaggt tgatgacgac 420
agacagtcag agttggggcg ttcaccaacc attccacca ccattccgaa tatcgcttcg 480
atcacatcgg caccatcaat caaaagccga tcatccatgc cgcctgcctt ccaatcccct 540
gggctacccc cacctgcac gcacgcccc ttcccaccca catcatatgc agcgtcgccc 600
ttgcacaaat ctttgacccc gccgccttat gaattctccc gcaaccgtga cgccgacct 660
gaacctttcc cctccattga atcgtctttg gactcagcat cgacaacatc tggaaagcac 720
ttttactcca accacttgaa ccccgccaga aatccagatt cgagtccagt gttaaactta 780
tttccatctt ccgcagccca gcgacaacac caccgcttct ctaatcccac cccggcgtct 840
ttccgtagca gggagataca gatcttctgc gccagctgca agcaggcatg gcctctcaat 900
gaatgctatg cctgtactga atgtatctgc ggggtatgcc gcgattgcgt cggaagtttc 960
atgagcagtc cgcctgcgac gttcaagaac gtgacatcca gccctgggag cgcaatgtca 1020
cacggcccca caagctatcc gagtccgaac ccacgtggtt gccacgctg ccacaccgtg 1080
ggaggggaagt ggaaagcatt ccaactggac atcaaa 1116

```

<210> 10

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 10

```

Met Ile Asn Glu Thr Gln Glu Ile His Ser Glu Asn Asp Ile Asp Arg
1           5           10           15
Ala Pro Met Arg Ser Ser Ile Glu Leu Pro Ser Leu Arg Asp His Phe
20           25           30
Lys Arg Asp Ser Leu Pro Pro Phe Ser Ser Pro Gln Pro Arg Ser Leu
35           40           45
Leu Pro Ser Ile Leu Asn His Ser Pro Pro Gly Arg Ser Ser Thr Leu
50           55           60
Pro Pro Ile Gln Arg Thr Asn Lys Leu Pro Arg Pro Arg Lys Gly Ser
65           70           75           80
Ile Thr Gly Ala Arg Lys Ala Lys His Glu Arg Ser Arg Ser Lys Glu
85           90           95
Phe Gly Arg Arg Pro Ser Ile Gly Asp Arg Lys Ala Leu Ser Ala Glu
100          105          110
Pro Gln Thr Ala Ala Trp Ala Gln Gly Lys Arg Trp Glu Asp Leu Ile
115          120          125
Glu Ala Ala Thr Ser Ala Thr Glu Val Asp Asp Asp Arg Gln Ser Glu
130          135          140
Leu Gly Arg Ser Pro Thr Ile Pro Pro Thr Ile Pro Asn Ile Ala Ser
145          150          155          160
Ile Thr Ser Ala Pro Ser Ile Lys Ser Arg Ser Ser Met Pro Pro Ala
165          170          175
Phe Gln Ser Pro Gly Leu Pro Pro Pro Ala Ser His Arg Pro Phe Pro
180          185          190
Pro Thr Ser Tyr Ala Ala Ser Pro Leu His Lys Ser Leu Thr Pro Pro
195          200          205
Pro Tyr Glu Phe Ser Arg Asn Arg Asp Ala Asp Leu Glu Pro Phe Pro

```

210		215		220
Ser Ile Glu Ser Ser Leu Asp Ser Ala Ser Thr Thr Ser Gly Lys His				
225		230		235
Phe Tyr Ser Asn His Leu Asn Pro Ala Arg Asn Pro Asp Ser Ser Pro				
	245		250	255
Val Leu Asn Leu Phe Pro Ser Ser Ala Ala Gln Arg Gln His His Arg				
	260		265	270
Phe Ser Asn Pro Thr Pro Ala Ser Phe Arg Ser Arg Glu Ile Gln Ile				
	275		280	285
Phe Cys Ala Ser Cys Lys Gln Ala Trp Pro Leu Asn Glu Cys Tyr Ala				
	290		295	300
Cys Thr Glu Cys Ile Cys Gly Val Cys Arg Asp Cys Val Gly Ser Phe				
305		310		315
Met Ser Ser Pro Pro Ala Thr Phe Lys Asn Val Thr Ser Ser Pro Gly				
	325		330	335
Ser Ala Met Ser His Gly Pro Thr Ser Tyr Pro Ser Pro Asn Pro Arg				
	340		345	350
Gly Cys Pro Arg Cys His Thr Val Gly Gly Lys Trp Lys Ala Phe Gln				
	355		360	365
Leu Asp Ile Lys				
370				

<210> 11
 <211> 933
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 11
 atgacggcgc gccaatcaac accgtcctcc gacaactcgc actcagacag cggcgtccgc 60
 aagcgagtagt gcaaggcttg cgatcggttg cgactgaaaa agtccaagtg tgacggagcc 120
 aaaccatgcg gtcgctgtcg agcagacaac acgctctgtg ttttcggcga gaggaagaaa 180
 gctcatgaca aagtgtaccc taaggggtat gttgagatgc tggaacaaca acaaacttgg 240
 ctagtcaatg gcctgcaaga actgtatcgc cgcttcttg aggggtgatg atggccgggc 300
 gagccgctga aatgcgaagc gaacgggcag cccttgacac acgatctctt gacgcagctc 360
 ggcgctctcg acacaagcaa gcacgagcgg ttcgaagaac acgccgaggt catgcagcag 420
 gaattatgga agcgaatgc cggacacatg cagcgccagg actcatcaga taccagctcc 480
 gagagccac agtcgccgt catgcggtct caattctcag atcccttttc tgtgcgaca 540
 gtaccacaaa ctccgacaac gatcagcccg aacacgacgc tgcgaataga cgtcccgcaa 600
 tcagcgacga agagtgaacc gcagatgaca tcgccaaact ccatatacac cacagccgtg 660
 tccatgccgc gagtggtcga ccgctctgag ctgcagagcg cccaaatagc aaaccgcag 720
 tggccagcc ctggctttgg aggtacgac gaaatggacc tgatgtctgg gcaatacaat 780
 ggtctgccat acgaagatgc gatctcctcg ccaatgttca atcgtccaat gccaatgggg 840
 tgcttgatac cagggtcata cggaacttg gataacaaga acgactttga ggatatcaac 900
 caatttctga acacacagtt ggagattacg tcg 933

<210> 12
 <211> 311
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 12

```

Met Thr Ala Arg Gln Ser Thr Pro Ser Ser Asp Asn Ser His Ser Asp
 1          5          10          15
Ser Gly Val Arg Lys Arg Val Cys Lys Ala Cys Asp Arg Cys Arg Leu
 20          25          30
Lys Lys Ser Lys Cys Asp Gly Ala Lys Pro Cys Gly Arg Cys Arg Ala
 35          40          45
Asp Asn Thr Leu Cys Val Phe Gly Glu Arg Lys Lys Ala His Asp Lys
 50          55          60
Val Tyr Pro Lys Gly Tyr Val Glu Met Leu Glu Gln Gln Gln Thr Trp
 65          70          75          80
Leu Val Asn Gly Leu Gln Glu Leu Tyr Arg Arg Leu Leu Glu Gly Asp
 85          90          95
Gly Trp Pro Gly Glu Pro Leu Lys Cys Glu Ala Asn Gly Gln Pro Leu
100          105          110
Thr His Asp Leu Leu Thr Gln Leu Gly Ala Leu Asp Thr Ser Lys His
115          120          125
Glu Arg Phe Glu Glu His Ala Glu Val Met Gln Gln Glu Leu Trp Lys
130          135          140
Arg Asn Ala Gly His Met Gln Arg Gln Asp Ser Ser Asp Thr Ser Ser
145          150          155          160
Glu Ser Pro Gln Ser Pro Val Met Pro Ser Gln Phe Ser Asp Pro Phe
165          170          175
Ser Val Arg Thr Val Pro Gln Thr Pro Thr Thr Ile Ser Pro Asn Thr
180          185          190
Thr Leu Arg Ile Asp Val Pro Gln Ser Ala Thr Lys Ser Glu Pro Gln
195          200          205
Met Thr Ser Pro Asn Ser Ile Tyr Thr Thr Ala Val Ser Met Pro Arg
210          215          220
Val Val Asp Pro Ser Glu Leu Gln Ser Ala Gln Ile Ala Asn Pro Gln
225          230          235          240
Trp Pro Ser Pro Gly Phe Gly Gly Tyr Asp Glu Met Asp Leu Met Ser
245          250          255
Gly Gln Tyr Asn Gly Leu Pro Tyr Glu Asp Ala Ile Ser Ser Pro Met
260          265          270
Phe Asn Arg Pro Met Pro Met Gly Cys Leu Ile Pro Gly Ser Tyr Gly
275          280          285
Asn Leu Asp Asn Lys Asn Asp Phe Glu Asp Ile Asn Gln Phe Leu Asn
290          295          300
Thr Gln Leu Glu Ile Thr Ser
305          310

```

<210> 13

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 13

```

atgtcgcagc ccatacgctg cootccaatg gagcactcgc cctcctcctt gtctcctac 60
tcctcttact cccccagttc gtectactcc gccgtgagcg acgactcggg catgagcatg 120
ttggacatgt acttcctgca cgggtggcgt ggacacggcg ccagccccgg cacaagcacg 180
gggtcccgga gcgtcgtcga tttcccgttc agccagcaat cgttcgattt cgagccttcg 240
tcgctggaca gcaatggccc ctacttcgag ttcaaccgga ctttcgtata cacacccgag 300

```

```

gcgtttcccg tcatggacgc cccgacctcc taccgcggcga gctcgaaccc ggcctgggtcg 360
ccaacctcca tgcttggtcga gcagtcgata tttcctctcg acgggcttag ccaagaacca 420
gtcaagccag ccaaacccta cagctgcgaa gattgcggca aggccttcac ccgcccagcg 480
gacctaaagc gccaccatag cactgtacac tacccggttt tccagaactg ccctgtaccg 540
gactgctcgc gcaaggacaa ccatggcttt ccgcggcgcg accacctcgt cgagcacctg 600
cgctcgtacc accacatgga tgtgccgaag cggcgcgcag caaagcgatt gagaactgtt 660

```

<210> 14
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 14
Met Ser Gln Pro Ile Ala Cys Pro Pro Met Glu His Ser Pro Ser Ser
 1           5           10           15
Leu Ser Ser Tyr Ser Ser Tyr Ser Pro Ser Ser Ser Tyr Ser Ala Val
          20           25           30
Ser Asp Asp Ser Gly Met Ser Met Leu Asp Met Tyr Phe Leu His Gly
          35           40           45
Gly Arg Gly His Gly Ala Ser Pro Gly Thr Ser Thr Gly Pro Gly Ser
          50           55           60
Val Val Asp Phe Pro Phe Ser Gln Gln Ser Phe Asp Phe Glu Pro Ser
65          70          75          80
Ser Leu Asp Ser Asn Gly Pro Tyr Phe Glu Phe Asn Pro Thr Phe Val
          85          90          95
Tyr Thr Pro Glu Ala Phe Pro Val Met Asp Ala Pro Thr Ser Tyr Pro
          100          105          110
Ala Ser Ser Asn Pro Ala Trp Ser Pro Thr Ser Met Leu Val Glu Gln
          115          120          125
Ser Ile Phe Pro Leu Asp Gly Leu Ser Gln Glu Pro Val Lys Pro Ala
          130          135          140
Lys Pro Tyr Ser Cys Glu Asp Cys Gly Lys Ala Phe Thr Arg Pro Ala
145          150          155          160
Asp Leu Lys Arg His His Ser Thr Val His Tyr Pro Val Phe Gln Asn
          165          170          175
Cys Pro Val Pro Asp Cys Ser Arg Lys Asp Asn His Gly Phe Pro Arg
          180          185          190
Arg Asp His Leu Val Glu His Leu Arg Ser Tyr His His Met Asp Val
          195          200          205
Pro Lys Arg Arg Ala Ala Lys Arg Leu Arg Thr Val
          210          215          220

```

<210> 15
 <211> 684
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 15
atgcttgctgc agaataacat ccagaaccag cagcagcagc agatgatgca gcagcagcag 60

```

```

cagcaacaac aacaacaaca acaacaacaa aatcaccaga atcaacaaca gaagtttgcc 120
aatccccagg cataccaggc tcagatgatg cgcgcgcaac tcatgcagat gcagctcgcc 180
caacagcagc agcaacaaag gcaacagcaa tcacaacagc agcaacaagc gcagccgcaa 240
ggccagcaac agccacagca tcaacaagga caaatgcttc aaaacagccc tcagctcaac 300
gcccagcaac agcagatggt gatggcagcg gcacaagcta acggcggcca actcccgcaa 360
aacatgcagg gcatgggtat gcagccgcca atgagtactc cagcgcggtg caaccagctc 420
tatcagcagc ggcttttgag actacggcaa gacatggcta cgcgtctgat gccacagtac 480
ggaccacca cgcaatatcc gccacaggtt gcgcaggagt acagtgttgg ccttgaaaac 540
gctgctaagg gcttcgtgca agacctcatt cgcagggagc gtgtcgagtt tgctgctgct 600
caacagcgac aagcccaggc tgctgcccac gcccaggcag tgcagcaaca gcagcacaac 660
atgatgcaga atggaatggg caag                                     684

```

<210> 16

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 16

```

Met Leu Ala Gln Asn Asn Ile Gln Asn Gln Gln Gln Gln Met Met
 1          5          10          15
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Asn His
      20          25          30
Gln Asn Gln Gln Gln Lys Phe Ala Asn Pro Gln Ala Tyr Gln Ala Gln
      35          40          45
Met Met Arg Ala Gln Leu Met Gln Met Gln Leu Ala Gln Gln Gln Gln
      50          55          60
Gln Gln Arg Gln Gln Gln Ser Gln Gln Gln Gln Gln Ala Gln Pro Gln
      65          70          75          80
Gly Gln Gln Gln Gln Pro Gln His Gln Gln Gly Gln Met Leu Gln Asn Ser
      85          90          95
Pro Gln Leu Asn Ala Gln Gln Gln Gln Met Leu Met Ala Ala Ala Gln
      100          105          110
Ala Asn Gly Gly Gln Leu Pro Gln Asn Met Gln Gly Met Gly Met Gln
      115          120          125
Pro Arg Met Ser Thr Pro Ala Arg Tyr Asn Gln Leu Tyr Gln Gln Arg
      130          135          140
Leu Leu Arg Leu Arg Gln Asp Met Ala Thr Arg Leu Met Pro Gln Tyr
      145          150          155          160
Gly Pro Pro Thr Gln Tyr Pro Pro Gln Val Ala Gln Glu Tyr Ser Val
      165          170          175
Gly Leu Glu Asn Ala Ala Lys Gly Phe Val Gln Asp Leu Ile Arg Arg
      180          185          190
Glu Arg Val Glu Phe Ala Ala Ala Gln Gln Arg Gln Ala Gln Ala Ala
      195          200          205
Ala His Ala Gln Ala Val Gln Gln Gln Gln His Asn Met Met Gln Asn
      210          215          220
Gly Met Gly Lys
225

```

<210> 17

<211> 906

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 17

```

atgaacaacg acttcatgca aaacaacatt cgcagcgccc aggatgtgga acagattatt 60
tccaacatcc gattctccgg catgacgcct ctaggttccg ctctgagatc caaggtactt 120
gatcccatga tagtgggtcc agccagagca ggccgcctgc aaaagccggt tctcgtcatc 180
actatcaccg atggtcagcc cgctggagaa cctctggact ccgtcgctca gggaattcgc 240
tacgtgttg atgaggtttc gagatcccca tttggacgtg gtgcggttgc cttccagttc 300
tcgcaagtcg gaaacgacac caaggctcgg gacttcctcg gcagtctcga caacgacctt 360
agcattggtg gcctgatcga ctgcacctcc aactttgaag tagaacagga tgagatgtcc 420
cgtgctaacc cacctgtgca tctgactcgt gagctgtggt gcgcgaaact catgctcggc 480
tctatcgatt cctcgtaaga taccaaggac gagaggggta gtggcccatc tggtgctcct 540
cctgggcttc ctctggcca gtacggcgcc tatggtcagt caggaccggg atacggctca 600
tccgcacccat acaatcccg ccagcaacag ccgtacagcc ctgcttacct cccgcacagc 660
caagcgccctg gaggttatgc acagccacct ccccaaggcc agtacggcgg ctatagccaa 720
ccgggcccgg gatatggctc acccgcgccct tacagctccg gacaacaaca ggggtatggc 780
tctgtcctt acccaccgag cagccaagcg tctgggagct atggccagca acaatatgga 840
caacggcccc gatctcagcc tggttatccc ggccaacagc ctccgtacgg acagcagccc 900
aggtat                                     906

```

<210> 18

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 18

```

Met Asn Asn Asp Phe Met Gln Asn Asn Ile Arg Ser Ala Gln Asp Val
1      5      10      15
Glu Gln Ile Ile Ser Asn Ile Arg Phe Ser Gly Met Thr Pro Leu Gly
20     25     30
Ser Ala Leu Arg Ser Lys Val Leu Asp Pro Met Ile Val Gly Pro Ala
35     40     45
Arg Ala Gly Arg Leu Gln Lys Pro Val Leu Val Ile Thr Ile Thr Asp
50     55     60
Gly Gln Pro Ala Gly Glu Pro Leu Asp Ser Val Ala Gln Gly Ile Arg
65     70     75     80
Tyr Ala Val Asp Glu Val Ser Arg Ser Pro Phe Gly Arg Gly Ala Val
85     90     95
Ala Phe Gln Phe Ser Gln Val Gly Asn Asp Thr Lys Ala Arg Asp Phe
100    105    110
Leu Gly Ser Leu Asp Asn Asp Pro Ser Ile Gly Gly Leu Ile Asp Cys
115    120    125
Thr Ser Asn Phe Glu Val Glu Gln Asp Glu Met Ser Arg Ala Asn Pro
130    135    140
Pro Val His Leu Thr Arg Glu Leu Trp Cys Ala Lys Leu Met Leu Gly
145    150    155    160
Ser Ile Asp Ser Ser Tyr Asp Thr Lys Asp Glu Arg Gly Ser Gly Pro
165    170    175
Ser Gly Ala Pro Pro Gly Pro Pro Pro Gly Gln Tyr Gly Gly Tyr Gly
180    185    190
Gln Ser Gly Pro Gly Tyr Gly Ser Ser Ala Pro Tyr Asn Pro Gly Gln
195    200    205

```

```

Gln Gln Pro Tyr Ser Pro Ala Tyr Pro Pro His Ser Gln Ala Pro Gly
 210          215          220
Gly Tyr Ala Gln Pro Pro Gln Gly Gln Tyr Gly Gly Tyr Ser Gln
225          230          235          240
Pro Gly Pro Gly Tyr Gly Ser Pro Ala Pro Tyr Ser Ser Gly Gln Gln
          245          250          255
Gln Gly Tyr Gly Ser Ala Pro Tyr Pro Pro Ser Ser Gln Ala Ser Gly
          260          265          270
Ser Tyr Gly Gln Gln Gln Tyr Gly Gln Arg Pro Gly Ser Gln Pro Gly
          275          280          285
Tyr Pro Gly Gln Gln Pro Pro Tyr Gly Gln Gln Pro Arg Tyr
 290          295          300

```

<210> 19
 <211> 810
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 19
atgactagcc gtcagaatga atacttcata cccggagatg gtattagccg agaagtaatt 60
caggccgaca tctgccgtta ccttggaat gatgctttag taagacctgg aaaccacaat 120
ggtcgcgcgg gattcttcat tcgcgcttat cgaaacctca catcagaaat gattgctgat 180
ctcaaggcgg actccgcccg ctgggaagca gacgtcagaa gtcgtgctga ccaagggttat 240
ccccggggca gctacatcca ggactacagc tactctcaac ctagccgggc tacaccaacc 300
tactcaacct ctatgggaag ttccatgcac cctgaaatgt cccatggtca aggcccttct 360
cctcctacaa cctacgctgc tccgcgcgag cagtattctg agcagtatca ccaatctggc 420
taccagcaa cttcaagtcc gtcatactca aatgctccgt catatccttc aaaccactcg 480
ggctttggat ctggtcagcc cccataacct caacatatcc cctacagtgc tccaaccagg 540
cctcctgtga cttctgaggt ccacccttca tatacttaag ccagctctgg ctatggtttc 600
gagaatgggc gaaacaatgc ccctcggtac cctggtcctg gatatgatgc cgattctgat 660
tattctcctg ttactaccgg aatggcttat cctgctacca ctgcccctga tccacggata 720
ggaatggagc ccagatacac accggagtcc acatatgacc gcagtaggcc gcagccagca 780
agagaaagag aggctccccg ccgaacgcgg

```

<210> 20
 <211> 270
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 20
Met Thr Ser Arg Gln Asn Glu Tyr Phe Ile Pro Gly Asp Gly Ile Ser
 1          5          10          15
Arg Glu Val Ile Gln Ala Asp Ile Cys Arg Tyr Leu Gly Asn Asp Ala
          20          25          30
Leu Val Arg Pro Gly Asn His Asn Gly Arg Ala Gly Phe Phe Ile Arg
          35          40          45
Ala Tyr Arg Asn Leu Thr Ser Glu Met Ile Ala Asp Leu Lys Ala Asp
          50          55          60
Ser Ala Arg Trp Glu Ala Asp Val Arg Ser Arg Ala Asp Gln Gly Tyr
65          70          75          80

```

Pro	Arg	Gly	Ser	Tyr	Ile	Gln	Asp	Tyr	Ser	Tyr	Ser	Gln	Pro	Ser	Arg
			85					90					95		
Ala	Thr	Pro	Thr	Tyr	Ser	Thr	Ser	Met	Gly	Ser	Ser	Met	His	Pro	Glu
			100					105					110		
Met	Ser	His	Gly	Gln	Gly	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Ala	Ala	Pro
		115					120					125			
Pro	Gln	Gln	Tyr	Ser	Glu	Gln	Tyr	His	Gln	Ser	Gly	Tyr	Pro	Ala	Thr
	130					135					140				
Ser	Ser	Pro	Ser	Tyr	Ser	Asn	Ala	Pro	Ser	Tyr	Pro	Ser	Asn	His	Ser
145					150					155					160
Gly	Phe	Gly	Ser	Gly	Gln	Pro	Pro	Tyr	Pro	Gln	His	Ile	Pro	Tyr	Ser
			165					170						175	
Ala	Pro	Thr	Gln	Pro	Pro	Val	Thr	Ser	Glu	Val	His	Pro	Ser	Tyr	Thr
			180					185					190		
Tyr	Ala	Ser	Ser	Gly	Tyr	Gly	Phe	Glu	Asn	Gly	Arg	Asn	Asn	Ala	Pro
		195					200					205			
Arg	Tyr	Pro	Gly	Pro	Gly	Tyr	Asp	Ala	Asp	Ser	Asp	Tyr	Ser	Pro	Val
	210					215					220				
Thr	Thr	Gly	Met	Ala	Tyr	Pro	Ala	Thr	Thr	Ala	Pro	Asp	Pro	Arg	Ile
225					230					235					240
Gly	Met	Glu	Pro	Arg	Tyr	Thr	Pro	Glu	Ser	Thr	Tyr	Asp	Arg	Ser	Arg
			245					250						255	
Pro	Gln	Pro	Ala	Arg	Glu	Arg	Glu	Ala	Pro	Arg	Arg	Thr	Arg		
		260						265					270		

<210> 21

<211> 2082

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 21

```

atgacacacc gagattccga cttccgtcat caactgggca agtttcgact cgataccctg 60
ccgtcgcccc ctgtcgctgc tgtctgtgca cccccgtca tctcctccac ctccatcctc 120
tccagcccca acacgaccac caccaccacc accacaacaa cttcctcctc gggccccgtc 180
cgaagcaaaa gagtctccac cgcctgcatg ttctgtcgca aacgcaagaa gaaatgtgac 240
tttcgttatc ccaattgttc cgcctgtacg cgcgcggcg tgcatgtac cattccacca 300
cccgccctc aggtcgccag cgcctcgtc cctcgtgatc agctggaaac tctgcaaaat 360
cgcgtccgat ggctggaaga cgtggtgctc cggaagacgg gcatctctgt cgccgatcgg 420
cccacgggga cgcgctcga tggcgagggc gaccggact ggtggtacca ggtgccggcc 480
ttgatgatga cccgggacaa cctctccgc acggcgccgg ggacgaccgc gggaggcgtc 540
acctccagcc cgtctacctc gtctccatcc gccgtgggac ccgaattgcc caatgtcggc 600
gaaatcttcc gcgaccagct ggagcatcgt cgaccgtccg tggctcgtcc cgtcgccctc 660
gccccgcgcg tgtctcgact cgcctcgtc gcggaggcgg aacgcgtagc cgcacagtac 720
ttcgatagca tgggctatca atatccctt ctccatcgcg gggatttctt cgcgcagtgt 780
cgatcgcttt atacctccga cagcgtcgtt gcccgaggg tccactatac ctaccacatt 840
actatcgcca tctcgctcat catcggtcgt gccgacggc cacaggccat cgagttctat 900
cgggccaagt aggagacgtt ttcgatggca ttgcagaatg aggacctggc ggccgtccgc 960
gcgctgctaa gtatggcctt gtatacaatg tttgcaacaa gcggtccgag cgtgtggcat 1020
gtgttgggta ccgactgcg gctggccacc agtctggggc tgcacaaagc gcgaccgct 1080
gccagcttgg tggagagga gatggctaaa cgggccttct ggagttctgt caatctggac 1140
cgactgatcg ccagcacgtt aggacgacct cttggcttag cggacgagga catcaccgtg 1200
gggttgccac gcgagttcaa cgaggactgg accgagggcg ccgggtcgag tgccatgacc 1260
attccagtgc aggtggtgct actacgtcgg atcttttcgc gcatctaccg atatctgtac 1320

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caggacggtc aagcgccacc ctggcaaccg gatgaccaga ccatgcgccg ggggatccaa 1740
gcggttgtcg tctgatgga ggagtttggc aaacggcggc cgggggtgga acgtctggcg 1800
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catatgctgg tggcgccgcc ggtcccgtg gccccgggtg tggacgacgt gctgctgggtg 1980
gacgggtcag gcaatattcc cgtgatggat ccgtccatgg ccgaacaatt gttctattcg 2040
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<210> 22

<211> 694

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 22

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20      25      30
Leu Ile Ser Ser Thr Ser Ile Leu Ser Ser Pro Asn Thr Thr Thr Thr
35      40      45
Thr Thr Thr Thr Thr Thr Ser Ser Ser Gly Pro Val Arg Ser Lys Arg
50      55      60
Val Ser Thr Ala Cys Asp Phe Cys Arg Lys Arg Lys Lys Lys Cys Asp
65      70      75      80
Phe Arg Tyr Pro Asn Cys Ser Ala Cys Thr Arg Ala Gly Val Arg Cys
85      90      95
Thr Ile Pro Pro Pro Gly Pro Gln Val Ala Ser Ala Ser Val Pro Arg
100     105     110
Asp Gln Leu Glu Thr Leu Gln Asn Arg Val Arg Trp Leu Glu Asp Val
115     120     125
Val Arg Arg Lys Thr Gly Ile Ser Val Ala Asp Arg Pro Thr Gly Thr
130     135     140
Pro Leu Asp Gly Glu Gly Asp Pro Asp Trp Trp Tyr Gln Val Pro Ala
145     150     155     160
Leu Met Met Thr Arg Asp Asn Leu Ser Arg Thr Ala Pro Gly Thr Thr
165     170     175
Ala Gly Gly Val Thr Ser Ser Pro Ser Thr Ser Ser Pro Ser Ala Val
180     185     190
Gly Pro Glu Leu Pro Asn Val Gly Glu Ile Phe Arg Asp Gln Leu Glu
195     200     205
His Arg Arg Pro Ser Val Ala Arg Pro Val Ala Ser Ala Pro Arg Val
210     215     220
Leu Arg Leu Ala Ser Leu Ala Glu Ala Glu Arg Val Ala Ala Gln Tyr
225     230     235     240
Phe Asp Ser Met Gly Tyr Gln Tyr Pro Phe Leu His Arg Gly Asp Phe
245     250     255
Leu Ala Gln Leu Arg Ser Leu Tyr Thr Ser Asp Ser Val Val Ala Pro
260     265     270

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Glu Val His Tyr Thr Tyr His Ile Thr Ile Ala Ile Ser Leu Ile Ile
 275 280 285
 Gly Ser Ala Asp Gly Ala Gln Ala Ile Glu Phe Tyr Arg Ala Ser Gln
 290 295 300
 Glu Thr Phe Ser Met Ala Leu Gln Asn Glu Asp Leu Ala Ala Val Arg
 305 310 315 320
 Ala Leu Leu Ser Met Ala Leu Tyr Thr Met Phe Ala Thr Ser Gly Pro
 325 330 335
 Ser Val Trp His Val Leu Gly Thr Ala Leu Arg Leu Ala Thr Ser Leu
 340 345 350
 Gly Leu His Lys Ala Arg Pro Ala Ala Ser Leu Val Glu Glu Glu Met
 355 360 365
 Ala Lys Arg Ala Phe Trp Ser Leu Tyr Asn Leu Asp Arg Leu Ile Ala
 370 375 380
 Ser Thr Leu Gly Arg Pro Leu Gly Leu Ala Asp Glu Asp Ile Thr Val
 385 390 395 400
 Gly Leu Pro Arg Glu Phe Asn Glu Asp Trp Thr Glu Ala Pro Gly Ser
 405 410 415
 Ser Ala Met Thr Ile Pro Val Gln Val Val Arg Leu Arg Arg Ile Phe
 420 425 430
 Ser Arg Ile Tyr Arg Tyr Leu Tyr Asn Asn Gln Pro Pro Pro Leu Ser
 435 440 445
 Ser Glu Val Thr Ala Thr Leu Arg His Phe Arg Gln Glu Leu Asp Asp
 450 455 460
 Trp Arg Arg Ala Ala Pro Val Tyr Pro Pro Ala Leu Leu Tyr Ser Thr
 465 470 475 480
 Ser Tyr Tyr Asp Tyr Leu Phe Ala Thr Thr Val Leu Leu Met Tyr Arg
 485 490 495
 Pro Ser Pro Arg Asn Pro Thr Pro Asp Thr Leu Ser Ile Ile Ser Cys
 500 505 510
 Gly Asp Ala Ser Ile Gln Val Ile Arg Ser Tyr Trp Asp Ser Tyr Ser
 515 520 525
 Val Gly Lys Leu Lys Trp Ile Trp Leu Thr Leu Ser Gln Ile Tyr Phe
 530 535 540
 Ala Gly Ile Thr Ile Leu Trp Cys Leu His Gln Asn Leu Arg Ala Ile
 545 550 555 560
 Gln Asp Gly Gln Ala Pro Pro Trp Gln Pro Asp Asp Gln Thr Met Arg
 565 570 575
 Arg Gly Ile Gln Ala Val Val Val Leu Met Glu Glu Phe Gly Lys Arg
 580 585 590
 Arg Pro Gly Val Glu Arg Leu Ala Glu Thr Phe Arg Gln Gln Ser Thr
 595 600 605
 Thr Ile Phe Ser His Leu Val Ala Tyr Gln Pro Gln Pro Pro Gln
 610 615 620
 Ser Gln Pro Pro Ala Pro Pro Pro Leu Ser Gln Ser Gln Ser Gln Pro
 625 630 635 640
 His Met Leu Val Ala Pro Pro Val Pro Leu Ala Pro Val Leu Asp Asp
 645 650 655
 Val Leu Leu Val Asp Gly Ser Gly Asn Ile Pro Val Met Asp Pro Ser
 660 665 670
 Met Ala Glu Gln Leu Phe Tyr Ser Tyr Asp Trp Phe Gln Glu Glu Met
 675 680 685
 Ala Thr Phe Tyr Thr Leu
 690

<210> 23

<211> 1371
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 23
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 ggactccatc cgcaaataccc cgcacacctc atccaatctc tcctggccac gcacaaccac 180
 actaccacca gctgcccacac caccatcctt tcgcccgcgc agttcctcat tcccggattc 240
 atcgacaccc acattcacgc tccccaatgg agtcaacgcg gcgtggggcg gggcatccca 300
 ctgctcaact ggctggaggg gatcacgttc gcgcatgaag cgcgctgcag cgacgacgcc 360
 tacgcgcggc ggctcttcca ctctgtcgtg agcggcggcc tcaaacaagg cgtcacgaca 420
 gcctgtact acagttcgcg gcacgcctcg gcaacgggtc tcctggccga gacgtgtctc 480
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 ggtgggtttt cgtcgtcgat gctggatgtc atgcgcagtg cgtttatggt gagtgtggca 1080
 cgggagacgc agacggacgg ccgcgacaag ccgctgtctc ttgcggaggg gttctatctg 1140
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 ccagtggagg aggaggattc gctcgagacg gtgtttgaga agttcttgat gacgggggat 1320
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<210> 24
 <211> 457
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 24
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 20 25 30
 Ile Asp Gln His Gly Lys Ile Glu Gly Leu His Pro Gln Ile Pro Ala
 35 40 45
 Ser Ser Ile Gln Ser Leu Leu Ala Thr His Asn His Thr Thr Thr Ser
 50 55 60
 Cys Pro Thr Thr Ile Leu Ser Pro Ala Glu Phe Leu Ile Pro Gly Phe
 65 70 75 80
 Ile Asp Thr His Ile His Ala Pro Gln Trp Ser Gln Arg Gly Val Gly
 85 90 95
 Arg Gly Ile Pro Leu Leu Asn Trp Leu Glu Gly Ile Thr Phe Ala His
 100 105 110
 Glu Ala Arg Cys Ser Asp Asp Ala Tyr Ala Arg Arg Leu Phe His Ser
 115 120 125

Cys Val Ser Gly Gly Leu Lys Gln Gly Val Thr Thr Ala Cys Tyr Tyr
 130 135 140
 Ser Ser Arg His Ala Ser Ala Thr Val Ile Leu Ala Glu Thr Cys Leu
 145 150 155 160
 Ala Leu Gly Gln Arg Ala Leu Leu Gly Lys Cys Asn Met Asp Arg His
 165 170 175
 Ala Val Asp Trp Tyr Val Asp Glu Ser Ala Ala Ala Ser Val Ser Asp
 180 185 190
 Thr Glu His Val Ile Arg Ala Val Arg Ala Leu Asp Ala Glu His Gly
 195 200 205
 Leu Val Thr Pro Val Ile Thr Pro Arg Phe Ala Ile Ser Cys Ser Asp
 210 215 220
 Gly Leu Leu Arg Ala Leu Gly Glu Leu Ala Ala Arg Ala Glu Tyr Arg
 225 230 235 240
 Ala Leu Pro Ile Gln Thr His Phe Asn Glu Ser Arg Gln Glu Met Ala
 245 250 255
 Phe Thr Arg Ser Leu Phe Pro Gly Val Gln Asp Glu Thr Ala Leu Tyr
 260 265 270
 Glu Ser Phe Gly Leu Leu Asn Ser Arg Cys Val Leu Ala His Ala Ile
 275 280 285
 Tyr Leu Ser Pro Arg Glu Met Asp Arg Val Gln Ala Leu Asp Cys Gly
 290 295 300
 Ile Ala His Cys Pro Val Pro Asn Thr Thr Met Asp Glu Phe Met Val
 305 310 315 320
 Ala Pro Val Arg Glu Tyr Leu Ala Arg Gly Met Lys Val Gly Leu Gly
 325 330 335
 Thr Asp Cys Gly Gly Gly Phe Ser Ser Ser Met Leu Asp Val Met Arg
 340 345 350
 Met Ala Phe Met Val Ser Val Ala Arg Glu Thr Gln Thr Asp Gly Arg
 355 360 365
 Asp Lys Pro Leu Ser Leu Ala Glu Gly Phe Tyr Leu Ala Thr Ala Gly
 370 375 380
 Gly Ala Arg Val Cys Gly Leu Ala Glu Lys Val Gly Arg Phe Ala Val
 385 390 395 400
 Gly Met Glu Phe Asp Ala Val Leu Val Arg Thr Gly Asp Glu Val Asp
 405 410 415
 Gly Val Met Thr Pro Val Glu Glu Glu Asp Ser Leu Glu Thr Val Phe
 420 425 430
 Glu Lys Phe Leu Met Thr Gly Asp Asp Arg Asn Met Val Arg Val Phe
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 Val Lys Gly Arg Glu Val Arg Gly Leu
 450 455

<210> 25

<211> 2832

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 25

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 tcctcatcct ccccgcaatc cgcgtcgaag cgtctcccgg gcgccggcca aacttcttcg 180
 gctacctcga tggctggaac caccgcaa at ggcatcaatg gcacgacaga cgcgaagggt 240

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ccccgaatc gtccgaagag ggatgcgccg aagccagggg aggctgctgg ccggttacaa 300
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gaacctatg tgaaaacgac aaattacatc ctcaagaaat actccaaatg tcctccatcg 420
cttgctctcc accttcaccc cacacatttc cgcttcgaac aacaagatgg gagttttccg 480
tataactccg aaatgaagggt tgtcatcgaa catcttcgag ccggcactgt gcctcacgag 540
ataatagaag agctcctgag tgccaacatc cggttctatg aaggctgtct catcgtagcg 600
gtgattgacc acaagtctgt gtccgcgcag gcgcgaaaga cgacagcaca ttcattcaat 660
gaaaataaca cccctttctc gatccacaac tataacgaac acataacacc atctgcctat 720
gtcccgtatc ctaaacagaa tcaattaacc tccgagaaaag acgacacgaa ttctacagct 780
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cagcagatga tgatggcagc cgcccaagcc aacagcggac atccaccgca gaacatgcag 2520
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tgggtgagcg atatcatccg ccgagagcgt gaggcgcac agcaacaacg agcgaaccag 2760
gtcgtgccc tgcaagcgca agtcttgag cagcaacagc agcagaacat gatgcagaac 2820
ggcatgggca aa 2832

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<210> 26

<211> 944

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 26

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His Pro Pro Lys Met Lys Arg Pro Pro Pro Phe Val Gln Thr Gly

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Val	Asn	Gly	Val	Lys	Ala	Gln	Gln	Ser	Ser	Ser	Ser	Pro	Gln	Ser	Ala	
		35					40					45				
Ser	Lys	Arg	Leu	Pro	Gly	Ala	Gly	Gln	Thr	Ser	Ser	Ala	Thr	Ser	Met	
	50					55					60					
Ala	Gly	Thr	Thr	Ala	Asn	Gly	Ile	Asn	Gly	Thr	Thr	Asp	Ala	Lys	Gly	
65					70					75					80	
Pro	Leu	Asn	Arg	Pro	Lys	Arg	Asp	Ala	Pro	Lys	Pro	Gly	Glu	Ala	Ala	
				85					90					95		
Gly	Arg	Leu	Gln	Lys	Leu	Gln	Ser	Arg	Thr	Thr	Ser	Thr	Asp	Leu	Gly	
			100					105					110			
Gln	Arg	Ser	Ser	Lys	Gln	Cys	Ala	Glu	Pro	Tyr	Val	Lys	Thr	Thr	Asn	
		115					120					125				
Tyr	Ile	Leu	Lys	Lys	Tyr	Ser	Lys	Cys	Pro	Pro	Ser	Leu	Val	Leu	His	
	130					135					140					
Leu	His	Pro	Thr	His	Phe	Arg	Phe	Glu	Gln	Gln	Asp	Gly	Ser	Phe	Pro	
145					150					155					160	
Tyr	Asn	Ser	Glu	Met	Lys	Val	Val	Ile	Glu	His	Leu	Arg	Ala	Gly	Thr	
				165					170					175		
Val	Pro	His	Glu	Ile	Ile	Glu	Glu	Leu	Leu	Arg	Ala	Asn	Ile	Arg	Phe	
			180					185					190			
Tyr	Glu	Gly	Cys	Leu	Ile	Val	Arg	Val	Ile	Asp	His	Lys	Ser	Val	Ser	
		195					200					205				
Ala	Gln	Ala	Arg	Lys	Thr	Thr	Ala	His	Ser	Ser	Asn	Glu	Asn	Asn	Thr	
	210					215					220					
Pro	Phe	Ser	Ile	His	Asn	Tyr	Asn	Glu	His	Ile	Thr	Pro	Ser	Ala	Tyr	
225					230					235					240	
Val	Pro	Tyr	Pro	Lys	Gln	Asn	Gln	Leu	Thr	Ser	Glu	Lys	Asp	Asp	Thr	
				245					250					255		
Asn	Ser	Thr	Ala	Gly	Asn	Gln	Ala	Asp	Ala	Pro	Asn	Gly	Glu	Gln	Ser	
			260					265					270			
Ala	Ser	Ala	Lys	Asp	Gln	Gly	Asp	Ser	Gly	Ser	Ser	Gln	Gln	Asn	Glu	
		275					280					285				
Ala	Pro	Ser	Lys	Pro	Arg	Val	Phe	Thr	Thr	Val	Leu	His	Pro	Thr	Pro	
	290					295					300					
Arg	Ser	Leu	Gln	Ala	Glu	Leu	Thr	Leu	Leu	Ala	Thr	Thr	Pro	Ala	Arg	
305					310					315					320	
Thr	Ser	Pro	Ala	Asn	Ser	Thr	Thr	Arg	Thr	Gln	Gly	Ala	Ser	Met	Ala	
				325					330					335		
Pro	Pro	Ser	Pro	Gly	Gly	Ser	Asn	Thr	Gln	Leu	Asp	Arg	Gly	His	Val	
			340					345					350			
Ala	Lys	Lys	Gln	Lys	Met	Met	Val	Glu	Pro	Ala	Asp	Leu	Pro	Glu	Cys	
		355					360					365				
Glu	Ser	Arg	Leu	Thr	Arg	Ala	Leu	Ala	Pro	Pro	Leu	Phe	Leu	Asp	Pro	
	370					375					380					

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Met Gln His Glu Glu Lys Ala Lys Arg Glu His Glu Ile Lys Leu Lys
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Gln Glu Leu Ala Lys Arg Gln Gln Gln Glu Gln Glu Arg Glu Arg Arg
      500      505      510
Arg Ala Leu Glu Gln Arg Gln Ala Glu Glu His Ala Lys Asp Glu Ala
      515      520      525
Arg Arg Gln His Leu Ala Ala Gln Gln Gln Ala Gln Ala Gln Leu Ala
      530      535      540
Ala Gln Gln Gln Asn Arg His Val Met Ala Gln Ala Asn Gly Val Ser
545      550      555      560
Gln Ala Pro Gln Ser Ser Pro Val Val Arg Asn Gln Thr Pro His Asn
      565      570      575
Thr Ser Ser Pro Leu Val Gly Asn Ala Met Gly Thr Gln Ala Gly Val
      580      585      590
Pro Met Ser Met Thr Ser Ser Met Gln Gly Ala Gly Ser Pro Gln Arg
      595      600      605
Pro Pro Ser Ala Leu Gln His Ala His Pro Asn Leu Met Ser His Pro
      610      615      620
Met Ala Ala Ser Arg Ser Gln Gln Gly Pro Ser Arg His Gly Thr Pro
625      630      635      640
Gln Met Thr Gln Gly Thr Pro Ala Met Ser His Ala Thr Pro Ile Met
      645      650      655
Arg Asn Val Thr Pro Thr Gln Arg Met Ser His Ala Ser Pro Gly Arg
      660      665      670
Ser Thr Met Ala Pro Thr Pro Val Met Asn Gln Ala Met Met Gly Thr
      675      680      685
Pro Gln Met Ala Gly Gly Met Gly Leu Thr Pro Gln Gln Gln Gln Gln
      690      695      700
Met Leu Met Gln Gln Arg Gln Gln Leu Leu Ala Gln Gln Gly His Leu
705      710      715      720
Gly His Gly Gln Leu Thr Pro Gln Gln Tyr Ala Gln Leu Gln Ala Asn
      725      730      735
Ala His Ala Gln Gln Ser Ile Gln Ser His Pro Gln His Met Met Gln
      740      745      750
Ala Gln Gln Gln Asn Gln Gln Gln Pro Lys Ile Pro Asn Gln Gln Ala
      755      760      765
Tyr Gln Ser Gln Met Met Arg Ala Gln Leu Ala Gln Leu Gln Met Val
      770      775      780
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
785      790      795      800
Gln Gln Ser Gln Gly Gln Gln Ala His Val His Gln Gly Ser Pro Gln
      805      810      815
Met Asn Pro Gln Gln Gln Met Met Met Ala Ala Ala Gln Ala Asn Ser
      820      825      830
Gly His Pro Pro Gln Asn Met Gln Gly Val Ser Met Ala Gln Gly Ala
      835      840      845
Met Ala Gln Arg Tyr Asn Asn Met Tyr Gln Gln Arg Leu Leu Arg Leu
      850      855      860
Arg Gln Glu Met Ala Ser Lys Leu Met Pro Gln Tyr Gly Pro Pro Gly
865      870      875      880
Gln Tyr Pro Pro His Leu Leu Gln Gln Tyr His Ala Gly Leu Glu Arg
      885      890      895
Asn Ala Lys Ala Trp Val Ser Asp Ile Ile Arg Arg Glu Arg Glu Ala
      900      905      910
Ala Gln Gln Gln Arg Ala Asn Gln Val Ala Ala Val Gln Ala Gln Val
      915      920      925
Leu Gln Gln Gln Gln Gln Gln Gln Asn Met Met Gln Asn Gly Met Gly Lys

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930

935

940

<210> 27
 <211> 2043
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 27
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 tatctctacc aacatccgcc gttcgacatg gtcgacttct accccatcat ggactacgag 180
 gaatacgcag agaacctgtc ccgtccgata ttgaccaaag aacaagtcga gactctcgag 240
 gcccaattcc aggtcctatcc gaagcccagt agcaacgtca agcgccaatt ggccgctcaa 300
 acaaattctca gtcttccccc agtcgcgaac tggttccaaa acagacgggc caaagcgaag 360
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 tcgaagcgag gctcatcgga agagctggca agcacgcttg aaggcatcgg catccacacc 1080
 accgggtcga acggcctgtc acacctctcc acgggaccgg agcgtccac ctggagggaa 1140
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 acttcagatg ctctctcgat gctcgcggga tcgtcttcca tgtctccac gacaagagtg 1260
 ccgagctatg gcgccagtca cggagtgaga cagtcgaaat caacacaatg cctcaactcc 1320
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 gtcacgacgg gtgcattggc accaccaaca ccctgacgc ctgaagatct gcatcacctg 1500
 ctcccgaata ctcccaccga tgggggatac tgctgtcag cccaaccgac gagtgggttg 1560
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 gttgacctga tgtcgtctta cccgtacaac aacgtcgcgc ccccgatgtc tgcccctgcc 1680
 cattacacgt cgttcccaga gtacgtacac tgtgactcgg caaccatgac gggcgaggag 1740
 tggacagatg caacatcgat gccttctccg gaagcttcgt tccaaagtcg ctgtcccatg 1800
 ccgcagcagg cggatgggtc tatgtcgtat gagcgtctg tcgacacggt ccctatctca 1860
 gagtctccct ctttgggtgta ttcaactagc gagggcgacc tgtcgggtgca cgctgactcc 1920
 aaaggcatgg agttctgcat ccaggaattc cctgaacagc aagaagctca tcgattcggt 1980
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 ttc 2043

<210> 28
 <211> 681
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 28


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Met Asn Tyr Leu His Gln Pro Tyr Gln Tyr Val Ala His Pro Gly Ile
1      5      10      15
Pro Met Asp Gln Pro Met Ser Phe Asp Pro Thr Met Gly His Pro Ala
20      25      30
Met Met His Pro Met Asp Gly Gly Tyr Leu Tyr Gln His Pro Pro Phe
35      40      45
Asp Met Val Asp Phe Tyr Pro Ile Met Asp Tyr Glu Glu Tyr Ala Glu
50      55      60
Asn Leu Ser Arg Pro Ile Leu Thr Lys Glu Gln Val Glu Thr Leu Glu
65      70      75      80
Ala Gln Phe Gln Ala His Pro Lys Pro Ser Ser Asn Val Lys Arg Gln
85      90      95
Leu Ala Ala Gln Thr Asn Leu Ser Leu Pro Arg Val Ala Asn Trp Phe
100     105     110
Gln Asn Arg Arg Ala Lys Ala Lys Gln Gln Lys Arg Gln Glu Glu Phe
115     120     125
Glu Arg Met Gln Lys Ala Lys Ala Glu Ala Glu Glu Ala Ala Arg Gly
130     135     140
Lys Ser Glu Asn Glu Pro Asn Ala Glu Ser Thr Ser Asp Ser Lys Pro
145     150     155     160
Ser Thr Asp Asn Lys Thr Asp Lys Val Thr Pro Gln Gln Ser Ser Ser
165     170     175
Thr Asp Thr Thr Glu Asp Gln Ser Lys Thr Ala Ala Ser Ala Ser Ser
180     185     190
Ser Arg Ser Lys His Lys Lys Thr Arg Ser Glu Ser Ala Arg Glu Ala
195     200     205
Thr Phe Ala Ser Leu Gln Arg Ala Leu Asn Ala Ala Val Ala Ala Arg
210     215     220
Asp His Asn Ser Pro Asp Asn Glu His Arg Pro Ala Gly Asn Pro Asn
225     230     235     240
Ala Glu Gly Ser Ile Ser Pro Ala Thr Pro Phe Leu Asp Thr His Thr
245     250     255
Pro Gly His His Tyr Ala Asp Val Gln Ser Ala Gln Ser Ala Leu Asn
260     265     270
Thr Pro Tyr Pro Glu Trp Asp His Ser Lys His Trp Ala Pro Ser Gln
275     280     285
Ser Pro Ala Glu Ser Leu Gly Ser Gln His Thr His Asn Val Met Pro
290     295     300
Ser Val Gln Phe Pro Ser Ser Gln Ser Glu Glu Trp Ala Gly Gln Val
305     310     315     320
Gln Pro Thr Asp Asn Ser Phe His Thr Met Gln Tyr Pro Val Gln Pro
325     330     335
Glu Met Ala Leu Ser Lys Arg Gly Ser Ser Glu Glu Leu Ala Ser Thr
340     345     350
Leu Glu Gly Ile Gly Ile His Thr Thr Gly Ser Asn Gly Leu Ser His
355     360     365
Leu Ser Thr Gly Pro Glu Arg Pro Thr Trp Arg Glu Thr Gly Lys Glu
370     375     380
Leu Asp Leu Ala Ala Arg Arg Lys Arg Pro Arg Pro Ala Ala Ile Gly
385     390     395     400
Thr Ser Arg Ser Ser Ser Met Leu Ala Gly Ser Ser Ser Met Ser Pro
405     410     415
Thr Thr Arg Val Pro Ser Tyr Gly Ala Ser His Gly Val Arg Gln Ser
420     425     430
Lys Ser Thr Gln Cys Leu Asn Ser Arg Tyr Ala Gly Val Arg Lys Ala
435     440     445
Ser Ala Ala Gln Arg Ser Pro Leu Asn Leu Ser Asn Phe Ala Glu Ala

```

450		455		460	
Gly	Ala	Phe	Gly	Ser	Lys
465					470
Val	Thr	Thr	Gly	Ala	Leu
					485
Leu	His	His	Leu	Leu	Pro
					500
Ser	Ala	Gln	Pro	Thr	Ser
					515
Ile	Asn	Ile	Ala	Ser	Pro
					530
Ser	Ser	Tyr	Pro	Tyr	Asn
545					550
His	Tyr	Thr	Ser	Phe	Pro
					565
Thr	Gly	Arg	Ser	Trp	Thr
					580
Ser	Phe	Gln	Ser	Arg	Cys
					595
Ser	Tyr	Glu	Arg	Ser	Val
610					615
Leu	Val	Tyr	Ser	Thr	Ser
625					630
Lys	Gly	Met	Glu	Phe	Cys
					645
His	Arg	Phe	Val	Ala	Gln
					660
Phe	Asn	Asn	Gln	Thr	Pro
					675

<210> 29
 <211> 792
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 29	
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cagcagcaac	aaatgttgat
ggatcatggcc	agcttactcc
cagagtatcc	agtcgcaccc
ccaaagatac	cgaatcaaca
ttgcagatgg	tccagcaaca
caacagtccc	agggccagca
cagcagatga	tgatggcagc
ggagtaagca	tggcacaagg
ttgctacggt	tgaggcaaga
cagtacccac	cgcacctttt
tgggtgagcg	atatcatccg
gtcgtgccc	tgcaagcgca
ggcatgggca	aa

<210> 30
 <211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 30

```

Met Asn Gln Ala Met Met Gly Thr Pro Gln Met Ala Gly Gly Met Gly
 1           5           10           15
Leu Thr Pro Gln Gln Gln Gln Gln Met Leu Met Gln Gln Arg Gln Gln
          20           25           30
Leu Leu Ala Gln Gln Gly His Leu Gly His Gly Gln Leu Thr Pro Gln
          35           40           45
Gln Tyr Ala Gln Leu Gln Ala Asn Ala His Ala Gln Gln Ser Ile Gln
          50           55           60
Ser His Pro Gln His Met Met Gln Ala Gln Gln Gln Asn Gln Gln Gln
65           70           75           80
Pro Lys Ile Pro Asn Gln Gln Ala Tyr Gln Ser Gln Met Met Arg Ala
          85           90           95
Gln Leu Ala Gln Leu Gln Met Val Gln Gln Gln Gln Gln Gln Gln Gln
          100          105          110
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln Gly Gln Gln Ala
          115          120          125
His Val His Gln Gly Ser Pro Gln Met Asn Pro Gln Gln Gln Met Met
          130          135          140
Met Ala Ala Ala Gln Ala Asn Ser Gly His Pro Pro Gln Asn Met Gln
145          150          155          160
Gly Val Ser Met Ala Gln Gly Ala Met Ala Gln Arg Tyr Asn Asn Met
          165          170          175
Tyr Gln Gln Arg Leu Leu Arg Leu Arg Gln Glu Met Ala Ser Lys Leu
          180          185          190
Met Pro Gln Tyr Gly Pro Pro Gly Gln Tyr Pro Pro His Leu Leu Gln
          195          200          205
Gln Tyr His Ala Gly Leu Glu Arg Asn Ala Lys Ala Trp Val Ser Asp
          210          215          220
Ile Ile Arg Arg Glu Arg Glu Ala Ala Gln Gln Gln Arg Ala Asn Gln
225          230          235          240
Val Ala Ala Val Gln Ala Gln Val Leu Gln Gln Gln Gln Gln Gln Asn
          245          250          255
Met Met Gln Asn Gly Met Gly Lys
          260

```

<210> 31

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 31

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atgccgccac cagcctctgc agtggatttc tcgaatctac tgaacccccca aggcaacgcc 60
acctcttcca ctccctcgac tcccggtggac agctccaagg cgccgtccac tcctaccagt 120
gtcagtgcta acacgagtat ggccatcatc gtgagcctcc tccacacctc catgaaagga 180
gcgcgccccg ccaacgaaga agtccgccag gatcttcctc gcccttataa gtgccccctc 240
tgtgaccgtg ccttccaccg cttggaacac cagaccagac acatccgcac ccatacgggt 300

```

```

gaaaagccgc acgcatgcc a gttccccgga tgcacgaagc gtttcagtcg ctccgatgag 360
ctgacgcgcc actcccggat ccacaacaac cccaactccc gacgcagtaa caaggcgcaa 420
catctggccg ccgctgctgc tgccgcgcc gcgggtcagg acaatgcgat ggtcggcgcc 480
ccggcagggg ccatgatgcc tcctcccagc aagcccatca cgcggtccgc ccccgctctg 540
caggtgggat ccccggaagt gtccccgcct cattcgctact ccaactacgc cggtcacatg 600
cggtcgaact tgggaccgta tgcccgccac ggcgagcggg cgtcttcggg catggatatc 660
aacctcctcg cgaccgtgc ctgcgaagtc gagcgcgatg agcactacgc cttccacggt 720
ccccgtggtc acccgttctt tgccgcccgt catcacggcg gcaccggtcg tctcccgtcg 780
ctgtcggcct acgcgatctc gcacagcatg agtcgctcgc attcccacga ggatgacgat 840
gcttacacgc agcatcgctg gaagcgctcc cgccccaact cccccaactc gaccgcccc 900
tcctctccca ccttctcgca cgattcgctt tctcccacgc ccgaccacac tccgctggcg 960
accctgccc attcgccgcg gctgcggcct ctgggtgcc gtgaactgca tctgccttcg 1020
attcgccacc tgctgctcca tcacacgcc gcgctcgcgc ccatggagcc ccagccggag 1080
ggccccaact actacagccc tgcccagggt cagctgggtc ccagcatcag cgacatcatg 1140
tcgcgccccc acggcaccca gcgcaaactc cccgtccctc aggtgcccaa agtgcccggtg 1200
caggacatgc tgaatccggc gacgggattt tcgctcggtg cctcgtcgac gaacaactcc 1260
gtcgcgggtg gcgatctggc agaccgtttc 1290

```

<210> 32

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 32

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Met Pro Pro Pro Ala Ser Ala Val Asp Phe Ser Asn Leu Leu Asn Pro
1      5      10      15
Gln Gly Asn Ala Thr Ser Ser Thr Pro Ser Thr Pro Val Asp Ser Ser
      20      25      30
Lys Ala Pro Ser Thr Pro Thr Ser Ala Gln Ser Asn Thr Ser Met Ala
      35      40      45
Ser Ser Val Ser Leu Leu Pro Pro Leu Met Lys Gly Ala Arg Pro Ala
      50      55      60
Asn Glu Glu Val Arg Gln Asp Leu Pro Arg Pro Tyr Lys Cys Pro Leu
65      70      75      80
Cys Asp Arg Ala Phe His Arg Leu Glu His Gln Thr Arg His Ile Arg
      85      90      95
Thr His Thr Gly Glu Lys Pro His Ala Cys Gln Phe Pro Gly Cys Thr
      100     105     110
Lys Arg Phe Ser Arg Ser Asp Glu Thr Arg His Ser Arg Ile His
      115     120     125
Asn Asn Pro Asn Ser Arg Arg Ser Asn Lys Ala Gln His Leu Ala Ala
      130     135     140
Ala Ala Ala Ala Ala Ala Ala Gly Gln Asp Asn Ala Met Val Gly Ala
145     150     155     160
Pro Ala Gly Ala Met Met Pro Pro Pro Ser Lys Pro Ile Thr Arg Ser
      165     170     175
Ala Pro Val Ser Gln Val Gly Ser Pro Asp Val Ser Pro Pro His Ser
      180     185     190
Tyr Ser Asn Tyr Ala Gly His Met Arg Ser Asn Leu Gly Pro Tyr Ala
      195     200     205
Arg His Gly Glu Arg Ala Ser Ser Gly Met Asp Ile Asn Leu Leu Ala
      210     215     220
Thr Ala Ala Ser Gln Val Glu Arg Asp Glu His Tyr Gly Phe His Gly
225     230     235     240

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Pro	Arg	Gly	His	Pro	Phe	Phe	Ala	Pro	Arg	His	His	Gly	Gly	Thr	Gly
			245						250					255	
Arg	Leu	Pro	Ser	Leu	Ser	Ala	Tyr	Ala	Ile	Ser	His	Ser	Met	Ser	Arg
		260						265					270		
Ser	His	Ser	His	Glu	Asp	Asp	Asp	Ala	Tyr	Thr	Gln	His	Arg	Val	Lys
		275					280					285			
Arg	Ser	Arg	Pro	Asn	Ser	Pro	Asn	Ser	Thr	Ala	Pro	Ser	Ser	Pro	Thr
	290					295					300				
Phe	Ser	His	Asp	Ser	Leu	Ser	Pro	Thr	Pro	Asp	His	Thr	Pro	Leu	Ala
305					310					315					320
Thr	Pro	Ala	His	Ser	Pro	Arg	Leu	Arg	Pro	Leu	Gly	Ala	Ser	Glu	Leu
			325						330					335	
His	Leu	Pro	Ser	Ile	Arg	His	Leu	Ser	Leu	His	His	Thr	Pro	Ala	Leu
		340						345					350		
Ala	Pro	Met	Glu	Pro	Gln	Pro	Glu	Gly	Pro	Asn	Tyr	Tyr	Ser	Pro	Ala
		355					360					365			
Gln	Gly	His	Val	Gly	Pro	Ser	Ile	Ser	Asp	Ile	Met	Ser	Arg	Pro	Asp
	370					375					380				
Gly	Thr	Gln	Arg	Lys	Leu	Pro	Val	Pro	Gln	Val	Pro	Lys	Val	Ala	Val
385					390					395					400
Gln	Asp	Met	Leu	Asn	Pro	Ala	Thr	Gly	Phe	Ser	Ser	Val	Ser	Ser	Ser
			405						410					415	
Thr	Asn	Asn	Ser	Val	Ala	Gly	Gly	Asp	Leu	Ala	Asp	Arg	Phe		
		420						425					430		

<210> 33

<211> 3645

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 33

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atgaatcccg caaacttcaa cgtgggcggc tccatgcccg ccgcgcccac ccccagatg 60
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ggcacctata ccggttggcg cgccgaagtg cccatgaaag agcgcgtggt tcgagtgtat 180
caaatgttca cctcccttcg ccttatccaa cccaagcag atctgcaaca cctggcccaa 240
gctgcctca gctttgagca gaaggccttc aaagacgctc agcagaaagt cgattacgac 300
aaagaatgta acgacaaatt attgcatatt cgagatactc gagcgagaca ggccgccgctc 360
atgcagaatg gcatgattcc cccgggcgct cccaaagccg gcggcatgcg tggcgtcgga 420
caaccctcct tcccgcaaca gatgaatcga gccatgcaat ccaatcccat ggccggtcaa 480
caagccatgg ccatggggat gaccgatccg aatcaacagg ccgcatgcc gcagcgatcg 540
caacagcagc aagccatgat gcagcagcag cagcaacaac agcaacaaca gcaacagcag 600
cagcagcagc agcagccacg cgctcaacaa cgctccgcca ataccctcgc cctggtcgac 660
gagctgaata acctgactcc gcaagagtac gagaacgtca atcgcgtcgc tcaccagatc 720
atgaccaaga cctcgccggt ggatgcggag aaaatcaaac gcaacctgca gaacatgaat 780
cctgtacaac gccgttacct gactgaaaga aacatcgacc cggtcgcgta tttctttcgc 840
tcgcaggccc tcgcccacct caagcggcag atgaaggccc gtgtggacat gtctcacccc 900
cagaataccg gcgtcgaccc gaacaatgtg atgatggcg cccgatccgac gatgaacccc 960
cagatgttcc cgaacatgat gaacctacag cgcaattcgg ccttcgccat gggcaaccag 1020
ccaaacatgg acccctcttc cttcattggc aacgtggaga acatccaagg acagcaggcg 1080
gatggcctcc gttcgcagga agctggtcag ctggtcgtec ccgcgagctc ctcccagatg 1140
aaccaacaac cgttcaacaa cgcccagaac accttcccga tgggccaaca gctcgcgcag 1200
ggaggacagg ctaatctggg cgctgccggc atcaaccccc agatgttcgc ccaacaacac 1260
atgcaaaaaca ccccgaaatat gccgcgggat cgccccagc cggccgcccc tttccagccc 1320

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cagactcaag cacagaacca ggctcaggcc caggcccgcg cccaggcagc tcaaaaagcc 1380
cagatggcga tttcccaggc cggccaagct aattcgcaac tgcaacagcc catgccgcag 1440
caaagccctg ccatgcccac gttgaaccga cccatgcctc cgggccagat gtctcccgcg 1500
cagatggcag cgcaagtccg tcctccgtcg cgggcaccog ccatgggcca gcagccttcc 1560
atgggaggcc agcagcctat gcagggtcga ccgcaaatcc ccccgggtct cccccgggcc 1620
attcaagaac aactggcgca aatgtctcca gagcagctga accgggtctt ggcccagcgg 1680
cgcgccatgg cgaataatcc ggccctggcg agagccaacg cggcccggca atccgtgccc 1740
atgcagcaga gcgtgtccca gtccgcgcag gccagtcga tggcgaacaa ccagaacatg 1800
cgagcgatga atgtacaagc gcagctagct gggatgggog gggcgcaaca aatgatgcct 1860
ggtcaacaaa tgtccctcca acagcagcag cagcaacagc agcagcagca gcgtcaagag 1920
ctatataaga tgcagctact ccaacagtca ggcggtaatc tagagctctc gaatgagcaa 1980
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gtttcgctgg tgcccaagaa tatcaagacg tggggtcagc tcaaacagtg ggccgcgaca 2100
aatccacaaa tcccaggagg gctgaatctg cagaagttga tggccctcca gaaattccac 2160
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ggtccctgga tgtcggggccc gacacaagcc ccccagcaac cgccgatgat gaaccctcag 2280
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caaggggtgg cggtccttgc accctccaag cccaatatgc cattcaccag agagcagttg 2820
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acgaacctgc aacagctcca gcaacaagag gaagctctcc aacgggcgcg gcgagcgteg 3420
agccagaccg ccgtgtctgc aacatcggct gtcccacccg cccatttggt gcgcgcgtcc 3480
cctcagggcg ttcctcatgc gtacggggcg ggaagcatgc cgccggagca gttgaagttg 3540
cctccgccga agaagagaaa gcagtcccat ccaggggcta ccccaccgt cggcacgcct 3600
gctaccaagc cgccaaccac ccggcccgcg gacgtcaaaa tgccc 3645

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<210> 34

<211> 1215

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 34

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Met Asn Pro Ala Asn Phe Asn Val Gly Gly Ser Met Pro Ala Ala Pro
 1             5             10             15
Thr Pro Gln Met Pro Arg Leu Asp Asn Asn Gln Val Met Met Asn Tyr
             20             25             30
Val Ala Gln Ala Leu His Ala Gln Gly Thr Tyr Thr Gly Trp Arg Ala
             35             40             45
Glu Val Pro Met Lys Glu Arg Val Val Arg Val Tyr Gln Met Phe Thr
             50             55             60

```

```

Ser Leu Arg Leu Ile Gln Pro Gln Ala Asp Leu Gln His Leu Ala Gln
65          70          75          80
Ala Ala Leu Ser Phe Glu Gln Lys Ala Phe Lys Asp Ala Gln Gln Lys
85          90          95
Val Asp Tyr Asp Lys Glu Cys Asn Asp Lys Leu Leu His Ile Arg Asp
100        105        110
Thr Arg Ala Arg Gln Ala Ala Val Met Gln Asn Gly Met Ile Pro Pro
115        120        125
Gly Ala Pro Lys Ala Gly Gly Met Arg Gly Val Gly Gln Pro Ser Phe
130        135        140
Pro Gln Gln Met Asn Arg Ala Met Gln Ser Asn Pro Met Ala Gly Gln
145        150        155        160
Gln Ala Met Ala Met Gly Met Thr Asp Pro Asn Gln Gln Ala Ala Met
165        170        175
Pro Gln Arg Ser Gln Gln Gln Gln Ala Met Met Gln Gln Gln Gln Gln
180        185        190
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Arg Ala
195        200        205
Gln Gln Arg Ser Ala Asn Thr Leu Ala Leu Val Asp Glu Leu Asn Asn
210        215        220
Leu Thr Pro Gln Glu Tyr Glu Asn Val Asn Arg Val Ala His Gln Ile
225        230        235        240
Met Thr Lys Thr Ser Pro Val Asp Ala Glu Lys Ile Lys Arg Asn Leu
245        250        255
Gln Asn Met Asn Pro Val Gln Arg Arg Tyr Leu Thr Glu Arg Asn Ile
260        265        270
Asp Pro Val Ala Tyr Phe Phe Arg Ser Gln Ala Leu Ala His Leu Lys
275        280        285
Arg Gln Met Lys Ala Arg Val Asp Met Ser His Pro Gln Asn Thr Gly
290        295        300
Val Asp Pro Asn Asn Val Met Met Gly Ala Asp Pro Thr Met Asn Pro
305        310        315        320
Gln Met Phe Pro Asn Met Met Asn Leu Gln Arg Asn Ser Ala Phe Ala
325        330        335
Met Gly Asn Gln Pro Asn Met Asp Pro Ser Ser Phe Ile Gly Asn Val
340        345        350
Glu Asn Ile Gln Gly Gln Gln Ala Asp Gly Leu Arg Ser Gln Glu Ala
355        360        365
Gly Gln Leu Val Val Pro Ala Ser Ser Ser Gln Met Asn Gln Gln Pro
370        375        380
Phe Asn Asn Ala Gln Asn Thr Phe Pro Met Gly Gln Gln Leu Ala Gln
385        390        395        400
Gly Gly Gln Ala Asn Leu Gly Ala Ala Gly Ile Asn Pro Gln Met Phe
405        410        415
Ala Gln Gln His Met Gln Asn Thr Pro Asn Met Pro Pro Asp Arg Pro
420        425        430
Gln Pro Ala Ala Pro Phe Gln Pro Gln Thr Gln Ala Gln Asn Gln Ala
435        440        445
Gln Ala Gln Ala Arg Ala Gln Ala Ala Gln Lys Ala Gln Met Ala Ile
450        455        460
Ser Gln Ala Gly Gln Ala Asn Ser His Leu Gln Gln Pro Met Pro Gln
465        470        475        480
Gln Ser Pro Ala Met Pro Met Leu Asn Arg Pro Met Pro Pro Gly Gln
485        490        495
Met Ser Pro Ala Gln Met Ala Ala Gln Val Arg Pro Pro Ser Arg Ala
500        505        510
Pro Ala Met Gly Gln Gln Pro Ser Met Gly Gly Gln Gln Pro Met Gln

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			515					520					525			
Gly	Arg	Pro	Gln	Ile	Pro	Pro	Gly	Leu	Pro	Pro	Ala	Ile	Gln	Glu	Gln	
	530					535					540					
Leu	Ala	Gln	Met	Ser	Pro	Glu	Gln	Leu	Asn	Arg	Val	Leu	Ala	Gln	Arg	
545					550					555					560	
Arg	Ala	Met	Ala	Asn	Asn	Pro	Ala	Leu	Ala	Arg	Ala	Asn	Ala	Ala	Arg	
				565					570						575	
Gln	Ser	Val	Pro	Met	Gln	Gln	Ser	Val	Ser	Gln	Ser	Ala	Gln	Ala	Gln	
			580					585					590			
Ser	Met	Ala	Asn	Asn	Gln	Asn	Met	Arg	Ala	Met	Asn	Val	Gln	Ala	Gln	
		595					600					605				
Leu	Ala	Gly	Met	Gly	Gly	Ala	Gln	Gln	Met	Met	Pro	Gly	Gln	Gln	Met	
	610					615					620					
Ser	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Arg	Gln	Glu	
625					630					635					640	
Leu	Tyr	Lys	Met	Gln	Leu	Leu	Gln	Gln	Ser	Gly	Gly	Asn	Leu	Glu	Leu	
			645						650					655		
Ser	Asn	Glu	Gln	Ser	Lys	Glu	Met	Asp	Arg	Leu	His	Phe	Pro	Pro	Ser	
			660					665					670			
Leu	Leu	Gly	Asn	Asn	Pro	Asn	Ile	Val	Ser	Leu	Val	Pro	Lys	Asn	Ile	
		675					680					685				
Lys	Thr	Trp	Gly	Gln	Leu	Lys	Gln	Trp	Ala	Ala	Thr	Asn	Pro	Gln	Leu	
	690					695					700					
Pro	Gly	Gly	Leu	Asn	Leu	Gln	Lys	Leu	Met	Ala	Leu	Gln	Lys	Phe	His	
705					710					715					720	
Phe	Thr	Gln	Ile	Leu	Asn	Gln	Ser	Lys	Glu	Arg	Ser	Arg	Asn	Pro	Asp	
			725						730					735		
Gln	Ala	Gly	Gln	Gly	Pro	Trp	Met	Ser	Gly	Pro	Thr	Gln	Ala	Pro	Gln	
			740					745					750			
Gln	Pro	Pro	Met	Met	Asn	Pro	Gln	Gln	Phe	Pro	Pro	Gly	Gln	Gln	Gln	
		755					760					765				
Ala	Ala	Ile	Asn	Met	Ala	Ala	Ile	Arg	Pro	Val	Thr	Ala	Gln	Asp	Ile	
	770					775					780					
Gln	Ala	Ala	Arg	Gln	Arg	His	Pro	Ala	Met	Ala	Gln	Asn	Phe	Thr	Asp	
785					790					795					800	
Asp	Gln	Ile	Arg	Glu	Ser	Leu	Asn	Lys	Ala	Arg	Gln	Arg	Gln	Leu	Met	
			805						810					815		
Leu	Leu	Ala	Gln	Gln	Arg	Ala	Ala	Gln	Ala	Gln	Glu	Leu	Ala	Ala	Gln	
			820					825					830			
Gln	Gln	Gln	Thr	Gln	Ala	Leu	Gln	Gln	Thr	Pro	Val	Gly	Gly	Pro	Ala	
		835					840					845				
Pro	Gly	Pro	His	Leu	Arg	Pro	Glu	Gly	Pro	Gly	Gln	Pro	Ala	Thr	Gln	
	850					855					860					
Pro	Gln	Gln	Gln	Ser	Pro	Ala	Thr	Lys	Ala	Pro	Ser	Thr	Val	Pro	Gly	
865					870											

Glu Lys Ile Arg Gln Ala Tyr His Asp Thr Leu Lys Gln Ala Pro Pro
 980 985 990
 Met Lys Phe Ala Ala Ile Thr Pro Glu Gln His Ala Ala Met Asn Gln
 995 1000 1005
 Gln Leu Arg Asp Cys Thr Asp Met Leu Gly Arg Met Asp Thr Leu Val
 1010 1015 1020
 Gln Trp Phe Ala Lys Ile Pro Gly Gln Glu Lys Asn Val Arg Ser Leu
 1025 1030 1035 1040
 Leu Ala Met Arg Ile Gln Leu Met Arg Gln Phe Lys Asn Ser Pro Asp
 1045 1050 1055
 Trp Val Leu Asn Asp Ser Leu Thr Ile Ser Pro Glu Asn Leu Thr Ala
 1060 1065 1070
 Thr Ile Asn Tyr Ile Lys Lys Leu Phe His Ala Met Ile Thr Arg Val
 1075 1080 1085
 Ser Gln His Gln Asn Gln Ala Pro Gly Gln Arg Pro Gly Gly Pro Gln
 1090 1095 1100
 Pro Pro Leu Thr Gln Ala Ser Gln Asn Ala Met Pro Ala Leu Asn Ala
 1105 1110 1115 1120
 Thr Asn Leu Gln Gln Leu Gln Gln Gln Glu Glu Ala Leu Gln Arg Ala
 1125 1130 1135
 Arg Arg Ala Ser Ser Gln Thr Ala Val Ser Ala Thr Ser Ala Val Pro
 1140 1145 1150
 Pro Ala Pro Phe Gly Ala Pro Ser Pro Gln Gly Val Pro His Ala Tyr
 1155 1160 1165
 Gly Pro Gly Ser Met Pro Pro Glu Gln Leu Lys Leu Pro Pro Pro Lys
 1170 1175 1180
 Lys Arg Lys Gln Ser His Pro Gly Ala Thr Pro Thr Val Gly Thr Pro
 1185 1190 1195 1200
 Ala Thr Lys Pro Pro Thr Thr Arg Pro Ala Asp Val Lys Met Pro
 1205 1210 1215

<210> 35
 <211> 1146
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 35
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 atccagtgtg tcgacaagcc gtctcgttgc ccgtgccttt gcggcgccag catgacctgc 120
 gactacatgg cgaccacccc agcgaactgg tccacgacta ccgagtcgcg gtcttcaccg 180
 gcgatgacct ccattgcgga ccccatgaac caccgcctcg ccacttcgcg gcctgcgggg 240
 gagctgaacc acaccgagct cgagctgatg gtgcaatggg gcaccgacac ctaccgttcc 300
 gtcgcgcacc agcccagcgt cgaatggatc tggcatgccg ccgtgcctcg ggaggccttg 360
 caacggccct ttctcctcca cggcctcctg gccgtctccg ccctgcacct cttcttccgc 420
 accaccggcg acacgcaggc aactacttg cgtaccgccc acgcccacg acaacacgcc 480
 gaggaaggcc tctcccaagc gctccgcgca ctggacgcct ccaactgcaa cgccgcgttc 540
 gccgtctgca gcatgctcac cgtcttctcc ttgtccctgc cgctggccgc gcgccgacc 600
 ccgacagccg cacacagtc cctggacgag ctgtgtcaca tcatgcggca cagcaccag 660
 tccatgagct ccctgtgcga gatcgtctac tgggtcggcc gcggcgacct ccacgcgctc 720
 atcgagtgcg acgaaaccgc acccgggatg ccggacacgt cgcggtctcg catcatggcg 780
 ttggcgcgcc tgaacgatac cctggcgacg caatccccgc agcacgagaa gcgcgtattc 840
 gaccgcgccc tcgacgcctt gggccactca ctcgaccagc tcgcccgcgg cggcgagctt 900
 ctctctctcg ccttcgggtg gattgtgcag atcccaccgc gggtcatcga gctcctccac 960

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gagcggcatc cgtttgcgct ggtgatacctg gcgcactatg cggtcgtcct gcatactgctg 1020
cgggagcggtt ggtgggtggg tgactggggc gcacgggtga ttcaagcggg gggacggagt 1080
ttagaatggg agtggagaaa ggcctggga tgggtgttg atgcgacggg atgtattctg 1140
ccgcaa 1146

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<210> 36

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 36

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 1          5          10          15
His Pro Gln Leu Ile Gln Cys Val Asp Lys Pro Ser Arg Cys Pro Cys
          20          25          30
Leu Cys Gly Ala Ser Met Thr Cys Asp Tyr Met Ala Thr Thr Pro Ala
 35          40          45
Asn Trp Ser Thr Thr Thr Glu Ser Ala Ser Ser Pro Ala Met Thr Ser
 50          55          60
Ile Ala Asp Pro Met Asn His Pro Leu Ala His Phe Ala Pro Ala Gly
 65          70          75          80
Glu Leu Asn His Thr Glu Leu Glu Leu Met Val Gln Trp Cys Thr Asp
          85          90          95
Thr Tyr Arg Ser Val Ala His Gln Pro Ser Val Glu Trp Ile Trp His
          100          105          110
Ala Ala Val Pro Arg Glu Ala Leu Gln Arg Pro Phe Leu Leu His Gly
          115          120          125
Ile Leu Ala Val Ser Ala Leu His Leu Phe Phe Arg Thr Thr Gly Asp
          130          135          140
Thr Gln Ala His Tyr Leu Arg Thr Ala His Ala His Arg Gln His Ala
          145          150          155          160
Glu Glu Gly Leu Ser Gln Ala Leu Arg Ala Leu Asp Ala Ser Asn Cys
          165          170          175
Asn Ala Ala Phe Ala Val Cys Ser Met Leu Thr Val Phe Ser Phe Ala
          180          185          190
Leu Pro Leu Ala Ala Arg Arg Thr Pro Thr Ala Ala His Ser Pro Leu
          195          200          205
Asp Glu Leu Cys His Ile Met Arg His Thr His Gln Ser Met Ser Ser
          210          215          220
Leu Cys Glu Ile Val Tyr Trp Val Gly Arg Gly Asp Leu His Ala Leu
          225          230          235          240
Ile Glu Cys Asp Glu Thr Ala Pro Arg Met Pro Asp Thr Ser Arg Leu
          245          250          255
Ala Ile Met Ala Leu Ala Arg Leu Asn Asp Thr Leu Ala Thr Gln Ser
          260          265          270
Pro Gln His Glu Lys Arg Val Phe Asp Arg Ala Leu Asp Ala Leu Gly
          275          280          285
His Ser Leu Asp Gln Leu Ala Arg Gly Gly Glu Leu Leu Ser Ala
          290          295          300
Phe Arg Trp Ile Val Gln Ile Pro Pro Arg Phe Ile Glu Leu Leu His
          305          310          315          320
Glu Arg His Pro Phe Ala Leu Val Ile Leu Ala His Tyr Ala Val Val
          325          330          335
Leu His Leu Leu Arg Glu Arg Trp Trp Val Gly Asp Trp Gly Ala Arg

```

			340					345					350			
Val	Ile	Gln	Ala	Val	Gly	Arg	Ser	Leu	Glu	Trp	Glu	Trp	Arg	Lys	Ala	
		355					360					365				
Leu	Gly	Trp	Val	Leu	Asp	Ala	Thr	Gly	Cys	Ile	Leu	Pro	Gln			
	370					375					380					

```
<210> 37
<211> 540
<212> DNA
<213> Artificial Sequence
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<220>
<223> fungal gene

<400>	37					
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ccgcagggtg	gttactccca	gggtggctat	ggtcagtccc	aggggtggtag	cgccaacgat	120
tactacggcg	gacagcagcc	tcagcatcac	cagcagcaag	gatacaacca	gtatgaccag	180
agccagcagg	gttatggtca	gcagcagcag	tatggtcagc	agcaatacgg	tcagcaaggt	240
catgatcaac	aggctcccgg	tgaagcccag	gagggcgagc	gtggactgat	gggcgctctg	300
gccggtggtg	cagcgggttg	tttcgcgggt	cacaaggcca	accacggctt	cctcggaacc	360
atcggcggtg	ccatcatggg	aagcatcgcg	gaagatgccg	tcaagaagca	caagaacaag	420
aacgagggtc	ccccgagta	cggcagcaac	tatggcggca	gccagtatgg	cggccctcct	480
ccctcccacg	gaggctctaa	caacggcatg	atggaccagc	tgggcagctt	cttcaagaaa	540

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<210> 38
<211> 180
<212> PRT
<213> Artificial Sequence
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<220>
<223> fungal gene

<400>	38															
Met	Ser	Gly	Tyr	Asn	Asn	Gln	Tyr	Asn	Gln	Gly	Tyr	Gly	Tyr	Asn	Gln	
1				5					10					15		
Gly	Gly	Tyr	Pro	Pro	Gln	Gly	Gly	Tyr	Ser	Gln	Gly	Gly	Tyr	Gly	Gln	
			20					25					30			
Ser	Gln	Gly	Gly	Ser	Ala	Asn	Asp	Tyr	Tyr	Gly	Gly	Gln	Gln	Pro	Gln	
		35					40					45				
His	His	Gln	Gln	His	Gly	Tyr	Asn	Gln	Tyr	Asp	Gln	Ser	Gln	Gln	Gly	
	50					55					60					
Tyr	Gly	Gln	Gln	Gln	Gln	Tyr	Gly	Gln	Gln	Gln	Tyr	Gly	Gln	Gln	Gly	
65					70					75					80	
His	Asp	Gln	Gln	Ala	Pro	Gly	Glu	Ala	Gln	Glu	Gly	Glu	Arg	Gly	Leu	
				85					90					95		
Met	Gly	Ala	Leu	Ala	Gly	Gly	Ala	Ala	Gly	Gly	Phe	Ala	Gly	His	Lys	
			100					105					110			
Ala	Asn	His	Gly	Phe	Leu	Gly	Thr	Ile	Gly	Gly	Ala	Ile	Met	Gly	Ser	
			115				120					125				
Ile	Ala	Glu	Asp	Ala	Ile	Lys	Lys	His	Lys	Asn	Lys	Asn	Glu	Gly	Pro	
	130					135					140					
Pro	Glu	Tyr	Gly	Ser	Asn	Tyr	Gly	Gly	Ser	Gln	Tyr	Gly	Gly	Pro	Pro	
145					150					155					160	
Pro	Ser	His	Gly	Gly	Ser	Asn	Asn	Gly	Met	Met	Asp	Gln	Leu	Gly	Ser	

165 170 175
Phe Phe Lys Lys
180

<210> 39
<211> 1191
<212> DNA
<213> Artificial Sequence

<220>
<223> fungal gene

<400> 39
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tgtgagaact gccgtcagtc gaaagtgaat tgcaacctgg gaggaagaa cacctgcatc 120
cgctgtcttc gccatggcct tccttgtcga taccgggtcg ccaaccgatc cggcaagccg 180
aaggggagca agaaccgagc tacgctgcga aagctgggccc agctccagga cgagaagccg 240
gtgcagggct cgcacagcgc gcgggagccg aagaaggccg tggagccggt gtgtccgccg 300
gagtatgagg tcgaccgcag attcgagtac cagacaagcg agccgagtcg gccgcggtcg 360
tctgagagtc cacatatgca cgactccac cgcacaatcg acgcctgcat gctagtgaat 420
gagacgcca tcgactacac ggctacctat ggcgcccggt tctccccgc catgccgatg 480
tgcacgccg cgctgatgtc gccgacatcg cccaccttc tgcaaaagga gttcatcacg 540
aaaggcctga ccagcttccc gctggccgtg cacgtccccg gcgccttacc gccgcgctgc 600
gagtgcgacg aggcgctcgg cttccacttg aacggactgc gacatatggt ggtcgacccg 660
gcgcggtgc gcttcgacca gggcctgcag gcgatcaaga cggcgctcgc cgtatgtcag 720
gggttcctgc ggtgcgcgcg ctgtccaaag ggcaacacga acttcctggt ctgcgtgtcg 780
acgctggacc tcgtgctgca gctcttcgac ttctgggtga gttgcgagtt cgcagccac 840
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tacgagacag cgcccagga ggcgcggcac atgcggcggg tgggtgctgc cgggcgctcg 960
ctgcagtga aggaggtgct gggcctgctg cacgaggccg tggagctggc cgagggccag 1020
ggcctgagca gtagcagcag cagtagcgag gcgctggacg ggagctggct gcagcagatc 1080
atccgcgggt atgcgagcgc gacggagtcc ctctccagc cgctggggtg tatttgcgga 1140
ggcagcgcg tgcaactagc gcatagaccg agtaccgggt tagataggct g 1191

<210> 40
<211> 397
<212> PRT
<213> Artificial Sequence

<220>
<223> fungal gene

<400> 40
Met Phe Ala Glu Ser Gln Pro Pro Ser Ser Gly Gly Asp Thr Pro Lys
1 5 10 15
Leu Arg Ala Ala Cys Glu Asn Cys Arg Gln Ser Lys Val Lys Cys Asn
20 25 30
Leu Gly Gly Lys Asn Thr Cys Ile Arg Cys Leu Arg His Gly Leu Pro
35 40 45
Cys Arg Tyr Arg Val Ala Asn Arg Ser Gly Lys Pro Lys Gly Ser Lys
50 55 60
Asn Arg Ala Thr Leu Arg Lys Leu Gly Gln Leu Gln Asp Glu Lys Pro
65 70 75 80
Val Gln Gly Ser His Ser Ala Arg Glu Pro Lys Lys Ala Val Glu Pro
85 90 95
Val Cys Pro Pro Glu Tyr Glu Val Asp Arg Arg Phe Glu Tyr Gln Thr

		100						105					110				
Ser	Glu	Pro	Ser	Gln	Pro	Arg	Leu	Ser	Glu	Ser	Pro	His	Met	His	Asp		
		115						120					125				
Ser	His	Pro	Thr	Ile	Asp	Ala	Cys	Met	Leu	Val	Asn	Glu	Thr	Pro	Ile		
		130					135					140					
Asp	Tyr	Thr	Ala	Thr	Tyr	Gly	Gly	Pro	Phe	Ser	Pro	Ala	Met	Pro	Met		
145						150				155					160		
Cys	Thr	Pro	Ala	Ser	Met	Ser	Pro	Thr	Ser	Pro	Thr	Phe	Leu	Gln	Lys		
				165					170					175			
Glu	Phe	Ile	Thr	Lys	Gly	Leu	Thr	Ser	Phe	Pro	Leu	Ala	Val	His	Val		
			180					185					190				
Pro	Gly	Ala	Leu	Pro	Pro	Arg	Cys	Glu	Cys	Asp	Glu	Ala	Leu	Gly	Phe		
		195					200					205					
His	Leu	Asn	Gly	Leu	Arg	His	Met	Val	Val	Asp	Pro	Ala	Arg	Leu	Arg		
		210				215					220						
Phe	Asp	Gln	Gly	Leu	Gln	Ala	Ile	Lys	Thr	Ala	Leu	Ala	Val	Cys	Gln		
225					230					235					240		
Gly	Phe	Leu	Arg	Cys	Ala	Arg	Cys	Pro	Lys	Gly	Asn	Thr	Asn	Phe	Leu		
				245					250					255			
Val	Ser	Leu	Ser	Thr	Leu	Asp	Leu	Val	Leu	Gln	Leu	Phe	Asp	Phe	Trp		
		260						265					270				
Val	Ser	Cys	Glu	Phe	Ala	Ala	His	Gly	His	Gly	His	Gly	Pro	Pro	Ala		
		275					280					285					
Ser	Ser	Leu	Glu	Ala	Glu	Pro	Met	Ala	Tyr	Gly	Glu	Tyr	Glu	Thr	Ala		
		290				295				300							
Pro	Glu	Glu	Ala	Arg	His	Met	Arg	Arg	Val	Val	Leu	Arg	Gly	Arg	Leu		
305					310					315					320		
Leu	Gln	Cys	Lys	Glu	Val	Leu	Gly	Leu	Leu	His	Glu	Ala	Val	Glu	Leu		
				325					330					335			
Ala	Glu	Gly	Gln	Gly	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Ala	Leu		
		340					345					350					
Asp	Gly	Ser	Trp	Leu	Gln	Gln	Ile	Arg	Gly	Tyr	Ala	Ser	Ala	Thr			
		355					360				365						
Glu	Ser	Leu	Leu	Gln	Pro	Leu	Gly	Cys	Ile	Cys	Gly	Gly	Ser	Ala	Val		
		370				375					380						
Gln	Leu	Ala	His	Arg	Pro	Ser	Thr	Gly	Leu	Asp	Arg	Leu					
385					390					395							

<210> 41

<211> 1155

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 41

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cgcgaccgca tgcgatcctc catcgagctc ccctctctgc gcgaccactt caagcaggac 180
tccctcccac ccttctcccc gcgaccgcgc gaactgctcc cctccatcct caaccactcg 240
ccccaggtc gctcctccac tcttcccccc atccagcaaa agaagtggcc gcgcccgcgc 300
aaatcctcca tctccggcgc tcgcaagccc aaacatgaac gctccaagtc caaggagtac 360
ggtcgcccgc ccagcttagg cgatcgcaaa gccctgtccg ccgaacccca gaccgccgcc 420
tggtcgcagg gcaagcgctg ggaggatctg atcgaagccg cgacttcggc gaccgaggcc 480
gacgacgaac gccattctga ggtcggctcg tcgcccacca tccctccggt gtccagcttc 540

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acctccgccc ccatggggaa gaatcgctcg tcgcttcccc cgggattcca aggactacca 600
ccccccacct cgcacgtgcc gttcccgcct catccctacg ccgcgtcgcc gttgaacaag 660
tccctgacct caccgccgta cgacctcgcg cgcagccggg acaatgacct ggagcccttc 720
ccctcgatag agtcgtccct cgactccgcc tcgaccgctg ccggaaagac cctccactat 780
aatcacgtcg gtccggccaa cgactccagt ccggtgctga acatgttccc gtcgtcggcc 840
gtgcagcgcc aacaccatcg cttttccaac cccacccccg cctccatgcg gagccgcgag 900
atccagatct attgcgcca ctgcaagcga ccgtgggcgc tcaacgaatg ctacgcctgc 960
accgagtgca tctgcggcgt ctgtcgcgaa tgtgtcggaa tgttcatcgg cagcccggcc 1020
acctccttcc gcaacgtcac ctccagcccg ggcagtgcct tgccccacgg cccgaccagc 1080
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<210> 42

<211> 385

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 42

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          20           25           30
Ser His Ser Asp Asn Asp Ile Ser Arg Asp Arg Met Arg Ser Ser Ile
          35           40           45
Glu Leu Pro Ser Leu Arg Asp His Phe Lys Gln Asp Ser Leu Pro Pro
 50           55           60
Phe Ser Pro Arg Pro Arg Glu Leu Leu Pro Ser Ile Leu Asn His Ser
65           70           75           80
Pro Pro Gly Arg Ser Ser Thr Leu Pro Pro Ile Gln Gln Lys Lys Trp
          85           90           95
Pro Arg Pro Arg Lys Ser Ser Ile Ser Gly Ala Arg Lys Pro Lys His
          100          105          110
Glu Arg Ser Lys Ser Lys Glu Tyr Gly Arg Arg Pro Ser Leu Gly Asp
          115          120          125
Arg Lys Ala Leu Ser Ala Glu Pro Gln Thr Ala Ala Trp Ala Gln Gly
          130          135          140
Lys Arg Trp Glu Asp Leu Ile Glu Ala Ala Thr Ser Ala Thr Glu Ala
145          150          155          160
Asp Asp Glu Arg His Ser Glu Val Gly Arg Ser Pro Thr Ile Pro Pro
          165          170          175
Val Ser Ser Phe Thr Ser Ala Pro Met Gly Lys Asn Arg Ser Ser Leu
          180          185          190
Pro Pro Gly Phe Gln Gly Leu Pro Pro Pro Thr Ser His Arg Pro Phe
          195          200          205
Pro Pro His Pro Tyr Ala Ala Ser Pro Leu Asn Lys Ser Leu Thr Pro
          210          215          220
Pro Pro Tyr Asp Leu Ala Arg Ser Arg Asp Asn Asp Leu Glu Pro Phe
225          230          235          240
Pro Ser Ile Glu Ser Ser Leu Asp Ser Ala Ser Thr Ala Ser Gly Lys
          245          250          255
Thr Leu His Tyr Asn His Val Gly Pro Ala Asn Asp Ser Ser Pro Val
          260          265          270
Leu Asn Met Phe Pro Ser Ser Ala Val Gln Arg Gln His His Arg Phe
          275          280          285

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Ser Asn Pro Thr Pro Ala Ser Met Arg Ser Arg Glu Ile Gln Ile Tyr
 290 295 300
 Cys Ala His Cys Lys Arg Pro Trp Ala Leu Asn Glu Cys Tyr Ala Cys
 305 310 315 320
 Thr Glu Cys Ile Cys Gly Val Cys Arg Glu Cys Val Gly Met Phe Ile
 325 330 335
 Gly Ser Pro Pro Thr Ser Phe Arg Asn Val Thr Ser Ser Pro Gly Ser
 340 345 350
 Ala Leu Pro His Gly Pro Thr Ser Tyr Pro Ser Ala Arg Gly Cys Pro
 355 360 365
 Arg Cys Arg Thr Val Gly Gly Lys Trp Lys Ala Phe Gln Leu Asp Phe
 370 375 380
 Lys
 385

<210> 43
 <211> 1395
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 43
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 cttccgccgc cctcgcttgg cggccatccc ggcttgcgcg ccagcaccaa caccaacatg 180
 aaccccttca cgttatccgg cacggggatc gcgaatggca tgtcggtcgc tgcgtttggc 240
 ggcgacggtg gaggcacggg ccttgccagt catgccgcgc agatgggggt cgcgagaggg 300
 gcacagatgc agcaacagca gttacatcag gccacgacg gccgactagc cctcgagacc 360
 aaagccggtg gcgtcaaaac gcggatacga gacgtatgga agcataatct tgctcaggaa 420
 atggcgatcc tcagacaact ggtggagaag tatccctaca tcagcatgga taccgagttt 480
 cccggcatcg tcgctcgctc cattggcgcc tttacgaata aagcggacta ccactaccaa 540
 acccttcgat gtaacgtcga cctgttgaag atgatccagc tgggaatcac ccttttttct 600
 tccgaaggag aagttcctcc ccccaatgcc accgatgcga atggacagcc gctcggaaac 660
 ggtctggtac ctgcgccctg cacctggcag ttcaacttcc ggttttcgtt ggaggatgac 720
 atgtacgccc aagagtcaac ggcgatgttg gcgaaggccg gtatcgattt cgccatgcac 780
 gacaagaatg gaatcgatcc ctttgagttc ggcgccctct tgatcagctc aggcctcgtc 840
 ctctcagatg acgtccaactg ggtttcgttc cactccggct acgatttcgg ctatttgatg 900
 aagattatgc tctgcaaacc tctcccggag aacgaagagg aatttcacag gcttctcaac 960
 atcttcttcc cgtcattata cgatattaaa tacctgatga agcatgcggg tcgcaatcaa 1020
 gccaaagtcc gattgcaaga tattgcggac gagctgggcg tcaagcgtgt cgggattgct 1080
 catcaggccg ggtcggactc gctcgtcacg ggcgagatct actggaagat gcgccagttg 1140
 gtcttcaacg gaaacatcga cgaagcgaaa tactccggtc agatctgggg gctgaacggc 1200
 caaatgccag cgtgctgta ttctatgcag ccccatcaga cccccaatct caacggggct 1260
 accatctatt cggccactgg cacccccagt acgccaatg ctgttcattc tgtcacgggc 1320
 agccacacac ccagcatgc actgacaccc ggtgccaccg gcgggggtgt gggacagttc 1380
 cagatggcaa agtca 1395

<210> 44
 <211> 465
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 44

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His	Leu	Gln	Gln	Ala	His	Leu	Gln	Gln	Gln	Gln	Pro	Gln	His	His	Pro		
			20					25					30				
His	Ala	Gln	Ser	Ala	Asn	Thr	Ala	Leu	Pro	Pro	Pro	Ser	Leu	Gly	Gly		
		35				40						45					
His	Pro	Gly	Phe	Ala	Ala	Ser	Thr	Asn	Thr	Asn	Met	Asn	Pro	Phe	Thr		
	50					55					60						
Leu	Ser	Gly	Thr	Gly	Ile	Ala	Asn	Gly	Met	Ser	Val	Ala	Ala	Phe	Gly		
65					70					75					80		
Gly	Asp	Gly	Gly	Gly	Thr	Gly	Leu	Ala	Ser	His	Ala	Ala	Gln	Met	Gly		
				85					90					95			
Phe	Ala	Arg	Gly	Ala	Gln	Met	Gln	Gln	Gln	Gln	Leu	His	Gln	Ala	His		
			100					105					110				
Asp	Gly	Arg	Leu	Ala	Leu	Glu	Thr	Lys	Ala	Gly	Gly	Val	Lys	Thr	Arg		
		115					120					125					
Ile	Arg	Asp	Val	Trp	Lys	His	Asn	Leu	Ala	Gln	Glu	Met	Ala	Ile	Leu		
	130					135					140						
Arg	Gln	Leu	Val	Glu	Lys	Tyr	Pro	Tyr	Ile	Ser	Met	Asp	Thr	Glu	Phe		
145					150					155					160		
Pro	Gly	Ile	Val	Ala	Arg	Pro	Ile	Gly	Ala	Phe	Thr	Asn	Lys	Ala	Asp		
				165					170					175			
Tyr	His	Tyr	Gln	Thr	Leu	Arg	Cys	Asn	Val	Asp	Leu	Leu	Lys	Met	Ile		
			180					185					190				
Gln	Leu	Gly	Ile	Thr	Leu	Phe	Ser	Ser	Glu	Gly	Glu	Val	Pro	Pro	Pro		
		195					200					205					
Asn	Ala	Thr	Asp	Ala	Asn	Gly	Gln	Pro	Leu	Gly	Asn	Gly	Leu	Val	Pro		
	210					215					220						
Ala	Pro	Cys	Thr	Trp	Gln	Phe	Asn	Phe	Arg	Phe	Ser	Leu	Glu	Asp	Asp		
225					230					235					240		
Met	Tyr	Ala	Gln	Glu	Ser	Thr	Ala	Met	Leu	Ala	Lys	Ala	Gly	Ile	Asp		
			245						250					255			
Phe	Ala	Met	His	Asp	Lys	Asn	Gly	Ile	Asp	Pro	Phe	Glu	Phe	Gly	Ala		
		260						265					270				
Leu	Leu	Ile	Ser	Ser	Gly	Leu	Val	Leu	Leu	Asp	Asp	Val	His	Trp	Val		
		275					280					285					
Ser	Phe	His	Ser	Gly	Tyr	Asp	Phe	Gly	Tyr	Leu	Met	Lys	Ile	Met	Leu		
	290					295					300						
Cys	Lys	Pro	Leu	Pro	Glu	Asn	Glu	Glu	Glu	Phe	His	Arg	Leu	Leu	Asn		
305					310					315					320		
Ile	Phe	Phe	Pro	Ser	Leu	Tyr	Asp	Ile	Lys	Tyr	Leu	Met	Lys	His	Ala		
			325						330					335			
Gly	Arg	Asn	Gln	Ala	Lys	Ser	Gly	Leu	Gln	Asp	Ile	Ala	Asp	Glu	Leu		
			340					345					350				
Gly	Val	Lys	Arg	Val	Gly	Ile	Ala	His	Gln	Ala	Gly	Ser	Asp	Ser	Leu		
		355					360					365					
Val	Thr	Gly	Glu	Ile	Tyr	Trp	Lys	Met	Arg	Gln	Leu	Val	Phe	Asn	Gly		
	370					375					380						
Asn	Ile	Asp	Glu	Ala	Lys	Tyr	Ser	Gly	Gln	Ile	Trp	Gly	Leu	Asn	Gly		
385					390					395					400		
Gln	Met	Pro	Ala	Leu	Leu	Tyr	Ser	Met	Gln	Pro	His	Gln	Thr	Pro	Asn		
			405						410					415			
Leu	Asn	Gly	Ala	Thr	Ile	Tyr	Ser	Ala	Thr	Gly	Thr	Pro	Ser	Thr	Pro		
			420					425				430					
Asn	Ala	Val	His	Ser	Val	Thr	Gly	Ser	His	Thr	Pro	Gln	His	Ala	Leu		

435 440 445
 Thr Pro Gly Ala Thr Gly Gly Val Leu Gly Gln Phe Gln Met Ala Lys
 450 455 460

Ser
465

<210> 45
 <211> 1518
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 45
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 tatctggcca tgcaattcga tccgaataaa cccggcgcac gagaccggtt tggtcgcacg 180
 ggggctttcg gtcccaatgg cgggtatccc cacgactcgg cccctctctg caaagttgtg 240
 attcaccatt tcacctgccg ctctttgacc atcggtagct ggcgccgcat tggacagaac 300
 gcgatggact tgggtggttt ctactcccc gagaaggctt gcatgacctt ctatatcaac 360
 aacgactcgg ccggctacaa aatcgagtac ccttttgctt acattaaaaa catcacgctg 420
 gaatcgggcg atcagacagc gcagcccaac ggagcgcccc cgcgcccggg cggctctcatt 480
 gttgaattga accgcccgcc gctcttctac atggattcct ccaactccgg tggcttctac 540
 cagtgcggcg acttcaccga ggaccagcag gccagccagc tgttggtgca ccatctcggc 600
 ggccaccca aagtccctgag cgtccagctg gccaagctgg tctcgttgga gtcgttccag 660
 aaccgtctgg cctacaacaa cttcgccatg agtgcgcccc tgtccccgcc ttttatccag 720
 cggcccgcct ccagcgcgaa tcagtttgcc cgggcgtttg tgggcatgta tgcggagAAC 780
 cccgcgacgc tgagcctgca gcaggcggcg cgcgacaca agcgccaacg cagccgttcg 840
 gtgccgtag ccgtcgactt ctcgcccatg cagaccccca tgctgtacca gatgcagAAC 900
 ccgtcgagc tcaaccagcc agattcgagt atctttgccc ccgttcgca gtcgacccat 960
 ccaactggcg tgaacctgcg catcgatagc tcggccccc acggcttcga cccgcgcggc 1020
 catcccatgt cggcgccac cacgaactca cctcggact ttgccagtcc ctgcgtattc 1080
 tcgacggggc ctccgggcca atccacgcc gtcgccacga gcatccacc gcaattcaac 1140
 atgccatttg tgtccccgcc ggtggactcg tctacgctcg ccaccagcg cgcgtcgcgc 1200
 tactccacgg tcagccacgc ggaccccatg attgcgcgac agtcccctcc catgaccaac 1260
 atgcatgcgt cgcaggagat gtacggcctg agcaacgagc atcaacccca ttttgcggaac 1320
 gagaacatgt ccatgagcgg catgttcccc aagcacaaca tgaatttctc ggtacccacc 1380
 acgatggacg tcggaggcaa cacctttgat cttcccatc agacctgtc caaccacccg 1440
 tccccggggg ttcagggtga ctaccaaagc atgactccgc tggagaatgt cgatcccaac 1500
 acgtgggctc ctggggcg 1518

<210> 46
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 46
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 1 5 10 15
 Ile Lys Met Leu Ala Lys Lys Ser Ile Glu Thr Gly Glu Gly Cys Asp
 20 25 30
 Ser Ile Pro Glu Ser Met Arg Gln Tyr Leu Ala Met Gln Phe Asp Pro

35					40					45					
Asn	Lys	Pro	Gly	Ala	Arg	Asp	Pro	Phe	Gly	Arg	Thr	Gly	Ala	Phe	Gly
50					55					60					
Pro	Asn	Gly	Gly	Tyr	Pro	His	Asp	Ser	Ala	Pro	Ser	Gly	Lys	Val	Val
65					70					75					80
Ile	His	His	Phe	Thr	Cys	Arg	Ser	Leu	Thr	Ile	Gly	Ser	Trp	Arg	Arg
				85					90					95	
Ile	Gly	Gln	Asn	Ala	Met	Asp	Leu	Val	Val	Phe	Tyr	Ser	Pro	Glu	Lys
			100					105					110		
Ala	Cys	Met	Thr	Tyr	Tyr	Ile	Asn	Asn	Asp	Ser	Ala	Gly	Tyr	Lys	Ile
		115					120					125			
Glu	Tyr	Pro	Phe	Ala	Tyr	Ile	Lys	Asn	Ile	Thr	Leu	Glu	Ser	Gly	Asp
		130					135					140			
Gln	Thr	Ala	Gln	Pro	Asn	Gly	Ala	Pro	Pro	Arg	Pro	Gly	Gly	Leu	Ile
145					150					155					160
Val	Glu	Leu	Asn	Arg	Pro	Pro	Leu	Phe	Tyr	Met	Asp	Ser	Ser	Asn	Ser
				165					170					175	
Gly	Gly	Phe	Tyr	Gln	Cys	Gly	Asp	Phe	Thr	Glu	Asp	Gln	Gln	Ala	Ser
			180					185					190		
Gln	Leu	Leu	Val	His	His	Leu	Gly	Gly	His	Pro	Lys	Val	Leu	Ser	Val
		195					200					205			
Gln	Leu	Ala	Lys	Leu	Val	Ser	Leu	Glu	Ser	Phe	Gln	Asn	Arg	Leu	Ala
		210					215				220				
Tyr	Asn	Asn	Phe	Ala	Met	Ser	Ala	Pro	Met	Ser	Pro	Pro	Phe	Ile	Gln
225					230					235					240
Arg	Pro	Ala	Ser	Gln	Pro	Asn	Gln	Phe	Ala	Pro	Ala	Phe	Val	Gly	Met
				245					250					255	
Tyr	Ala	Glu	Asn	Pro	Ala	Thr	Leu	Ser	Leu	Gln	Gln	Ala	Ala	Arg	Gly
			260					265					270		
His	Lys	Arg	Gln	Arg	Ser	Arg	Ser	Val	Pro	Val	Ala	Val	Asp	Phe	Ser
		275					280					285			
Ala	Met	Gln	Thr	Pro	Met	Ser	Tyr	Gln	Met	Gln	Asn	Pro	Ser	Gln	Phe
		290					295				300				
Asn	Gln	Pro	Asp	Ser	Ser	Ile	Phe	Ala	Pro	Val	Pro	Gln	Ser	Thr	His
305					310					315					320
Pro	Leu	Ala	Val	Asn	Leu	Arg	Ile	Asp	Thr	Ser	Ala	Pro	Tyr	Gly	Phe
				325					330					335	
Asp	Pro	Arg	Gly	His	Pro	Met	Ser	Ala	Ala	Thr	Thr	Asn	Ser	Pro	Ser
			340					345					350		
Asp	Phe	Ala	Ser	Pro	Ser	Leu	Phe	Ser	Thr	Gly	Pro	Pro	Gly	Glu	Ser
		355					360					365			
Thr	Pro	Val	Ala	Thr	Ser	Ile	His	Pro	Gln	Phe	Asn	Met	Pro	Phe	Val
		370					375				380				
Ser	Pro	Pro	Val	Asp	Ser	Ser	Thr	Leu	Ala	Thr	Gln	Ala	Ala	Ser	Pro
385					390					395					400
Tyr	Ser	Thr	Val	Ser	His	Ala	Asp	Pro	Met	Ile	Ala	Asp	Gln	Ser	Pro
				405					410					415	
Pro	Met	Thr	Asn	Met	His	Ala	Ser	Gln	Glu	Met	Tyr	Gly	Leu	Ser	Asn
			420					425					430		
Glu	His	Gln	Pro	His	Phe	Ala	Asp	Glu	Asn	Met	Ser	Met	Ser	Gly	Met
		435					440					445			
Phe	Pro	Lys	His	Asn	Met	Asn	Phe	Ser	Val	Pro	Thr	Thr	Met	Asp	Val
		450				455					460				
Gly	Gly	Asn	Thr	Phe	Asp	Leu	Pro	Ile	Gln	Thr	Leu	Ser	Asn	His	Pro
465					470					475					480
Ser	Pro	Gly	Val	Gln	Gly	Asp	Tyr	Gln	Ser	Met	Thr	Pro	Leu	Glu	Asn
				485					490					495	

Val Asp Pro Asn Thr Leu Ala Pro Gly Ala
500 505

<210> 47
<211> 1731
<212> DNA
<213> Artificial Sequence

<220>
<223> fungal gene

<400> 47
atgatgccag cgcaaatgcg gcagcttaac atgagaggaa atgcaatggg tcctcccaac 60
cttcagaaga gtgtgctgca gaacaatacc tctggcctct ctcaacaaca aatcgcccaa 120
ctccagaaga accaacattht gcagatgatg cagatgcaaa gagatcagtc cgagatggac 180
atgaatggte accgtcccca gtcccctgct tctgcccaga acgccccttc cccatccaag 240
cggccccgtc tggaaggcgg accgatgaac ggacaacagt tagcgcctaa cggacgtggg 300
caagcacagg gaatgcccgg tcaaccgaat ccgcaggccc tttttatgca gaatgggggt 360
ctcaaccac gaggaatgaa cccggcccaa ctacaggctt tccagcaggg tccgggcgcg 420
cagcagaaat caatccaggg catgccgaat ggcattatga atcccgggtg gatgccaaac 480
cagacggatc tgatgcccac gccagaaggc cagggtatgt acccgatgaa cggtgactac 540
tatggcgcgga atggtaaaat ggcccagggt cgggctggga tgcagacgcc tggcaatcag 600
ggaaaccatg ctcttcagga ttatcagatg cagcttatgt tgctggaaca gcagaataag 660
cgacgtttga tgatggctcg ccaagagcag gatagcatgg ctctgcctga cggccagccc 720
ccaatgcctg ggcagcagca gttgccgcca ggcacctctc cccaaggcag cagggcgggc 780
gcctctccga accccaacga tcagatgaag aggggtacac cgaagatgcc gcagaccggg 840
cttccaggct ctccgaatcc tggcgatgtc gctcaaggte gtggatcccc ggcttccatg 900
aatttcaaca gcgccagat gccaccgcag atgacgaacc cattcttcgc cgctccgaac 960
ggtatgcgac ccccgagctc gaaccgggca ttaccaccg gtccgcccag gggccagcaa 1020
attcctgcag gtgccagat gccgaatcgc gcttggcagc cgcagcaggg cgctcagggc 1080
caacctatgc cccacagca gtcccctgct gcgcagccgg ccacgggaac tccccaggaa 1140
cgcaaccaaa tgccgcccgc ccaggctcct cccgctgctg ggcctaattc cggacgcacg 1200
cagccgcccgt ctctcagac cggagccgct gcccttccca cgcgccagca atccaacaag 1260
gccgcacca aggggaagaa agacacgaag gacactaatc ggaagcggcc gaagaaggca 1320
gctggccctg cagcggtcgc agctgcctcg aatactgccg cgaacccctc gtccgaggct 1380
gagcatgcga cgacgcctgc gacgccgatc acgcctcagc atccgaactc gttcaacaag 1440
ccggggccca ataccacgac gactgcgccc cagcaacca catcggcgcc tgccgcaccg 1500
acgctggtgc agccgcgcgc acccgaccag aaccagccgt tcaatgacct tagcatgcca 1560
gacgcgtctg ctttcaacct ggacttcagc gccttgaga atccggacat tttggagaac 1620
ttcgaattcg atacctttct caacactgac gcgatacgg cgggggtttg gtttgatccc 1680
aacatgccat atcctgggga cggcgttgag actggtgccc gagaaggtct g 1731

<210> 48
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> fungal gene

<400> 48
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Val Pro Pro Asn Leu Gln Lys Ser Val Leu Gln Asn Asn Thr Ser Gly
20 25 30
Leu Ser Gln Gln Gln Ile Ala Gln Leu Gln Lys Asn Gln His Leu Gln

		35					40					45				
Met	Met	Gln	Met	Gln	Arg	Asp	Gln	Ser	Glu	Met	Asp	Met	Asn	Gly	His	
	50					55					60					
Arg	Pro	Gln	Ser	Pro	Ala	Ser	Ala	Glu	Asn	Ala	Pro	Ser	Pro	Ser	Lys	
65					70					75					80	
Arg	Pro	Arg	Leu	Glu	Gly	Gly	Pro	Met	Asn	Gly	Gln	Gln	Leu	Ala	Pro	
				85					90					95		
Asn	Gly	Arg	Gly	Gln	Ala	Gln	Gly	Met	Pro	Gly	Gln	Pro	Asn	Pro	Gln	
			100					105					110			
Ala	Leu	Phe	Met	Gln	Asn	Gly	Gly	Leu	Asn	Pro	Arg	Gly	Met	Asn	Pro	
		115					120					125				
Ala	Gln	Leu	Gln	Ala	Phe	Gln	Gln	Gly	Pro	Gly	Ala	Gln	Gln	Lys	Ser	
	130					135					140					
Ile	Gln	Gly	Met	Pro	Asn	Gly	Ile	Met	Asn	Pro	Gly	Val	Met	Pro	Asn	
145					150					155					160	
Gln	Thr	Asp	Leu	Met	Pro	Met	Pro	Glu	Gly	Gln	Gly	Met	Tyr	Pro	Met	
				165					170					175		
Asn	Gly	Asp	Tyr	Tyr	Gly	Ala	Asn	Gly	Gln	Met	Ala	Gln	Val	Arg	Ala	
			180					185					190			
Gly	Met	Gln	Thr	Pro	Gly	Asn	Gln	Gly	Asn	His	Ala	Leu	Gln	Asp	Tyr	
			195				200					205				
Gln	Met	Gln	Leu	Met	Leu	Leu	Glu	Gln	Gln	Asn	Lys	Arg	Arg	Leu	Met	
	210					215					220					
Met	Ala	Arg	Gln	Glu	Gln	Asp	Ser	Met	Ala	Arg	Pro	Asp	Gly	Gln	Pro	
225					230					235					240	
Pro	Met	Pro	Gly	Gln	Gln	Gln	Leu	Pro	Pro	Gly	Thr	Ser	Pro	Gln	Gly	
				245					250					255		
Ser	Arg	Ala	Gly	Ala	Ser	Pro	Asn	Pro	Asn	Asp	Gln	Met	Lys	Arg	Gly	
			260					265					270			
Thr	Pro	Lys	Met	Pro	Gln	Thr	Gly	Leu	Pro	Gly	Ser	Pro	Asn	Pro	Gly	
		275					280					285				
Asp	Val	Ala	Gln	Gly	Arg	Gly	Ser	Pro	Ala	Ser	Met	Asn	Phe	Asn	Ser	
	290					295					300					
Ala	Gln	Met	Pro	Pro	Asp	Met	Thr	Asn	Pro	Phe	Phe	Ala	Ala	Pro	Asn	
305					310					315					320	
Gly	Met	Arg	Pro	Pro	Ser	Ser	Asn	Pro	Ala	Phe	Thr	Thr	Gly	Pro	Pro	
				325					330					335		
Met	Gly	Gln	Gln	Ile	Pro	Ala	Gly	Ala	Gln	Met	Pro	Asn	Arg	Ala	Trp	
			340					345					350			
Gln	Pro	Gln	Gln	Gly	Ala	Gln	Gly	Gln	Pro	Met	Pro	Pro	Gln	Gln	Ser	
		355					360					365				
Pro	Ala	Ala	Gln	Pro	Ala	Thr	Gly	Thr	Pro	Gln	Glu	Arg	Asn	Gln	Met	
	370					375					380					
Pro	Pro	Pro	Gln	Ala	Pro	Pro	Ala	Ala	Gly	Pro	Asn	Ser	Gly	Arg	Thr	
385					390					395					400	

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Pro Ala Ala Pro Thr Leu Val Gln Pro Pro Pro Pro Asp Gln Asn Gln
    500                    505                    510
Pro Phe Asn Asp Leu Ser Met Pro Asp Ala Ser Ala Phe Asn Leu Asp
    515                    520                    525
Phe Ser Ala Leu Glu Asn Pro Asp Ile Leu Glu Asn Phe Asp Phe Asp
    530                    535                    540
Thr Phe Leu Asn Thr Asp Ala Asp Thr Ala Gly Phe Gly Phe Asp Pro
    545                    550                    555                    560
Asn Met Pro Tyr Pro Gly Asp Gly Val Glu Thr Gly Ala Gly Glu Gly
    565                    570                    575
Leu

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<210> 49
<211> 1152
<212> DNA
<213> Artificial Sequence

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<220>
<223> fungal gene

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<400> 49
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gggtatttcg aaagcctttt caatctccac aatctcatcc atgcgcagtc cgagttgggtc 180
cgcacacagg gtctcaattc gttctttgac caagtaggtc accaggagca tttgtacgag 240
atctttgtag atgcaaccga gagtgtcttt gagcaagtgt gtgaggcgat tcaggccggg 300
gtacggggacg attcgttcct gaaggatctc ttcaatgagg agttcaactc cagtgcggtc 360
atcacgcatt tcaggcttct taccagcgcc tggatgaaat tgaatcctca tcggtaccag 420
gccttctctgc cgctccccct cgatcagtac tgcacgacgc ggatcgagac cgtcaaaacg 480
gaaattgatg aagtgggcct ccaagctctg gtggacggcg tcatcgagcc gtccggcggt 540
gctgtcgaga tctgtacct ggaccggagt cagggcgaag cagtcactcc ccatctcttg 600
accccgagtc ggcctagcgc ttogacaatc cgtttgctgt atcgccctgg cactacgat 660
attgcgtacc aagcgaacc taccgtgaca atggaacca tcgtcaatta tcagtacggc 720
atgaccacca actactcgcc ctgggaccaa ggcgccctct cgtttgatgt gaactcgagt 780
ctcatgtcca ttcccaacct gatgatggac cctcctttg cgtctctccc ttcccccatg 840
actcccgctc cgagcccgta ccgcgtctcg cccctcagg aagtgttcca acctccgatg 900
cacacgcctc cgccaccggt ccccgctcgca tcgccgccac caccgcgat gtcagcccgc 960
ccccgatga cttcgttacc taaccggtcc tcagacgggc cgcagattcg actgaatccg 1020
ttggtgatga agcagaactt gagccactcg ctccccgtca cgactccatt caagaattcg 1080
ccgtacaacc aggcccattht ccaaaaccag gactttgagc caatccactg ggaaccag 1140
gattcccgca aa 1152

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<210> 50
<211> 384
<212> PRT
<213> Artificial Sequence

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<220>
<223> fungal gene

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<400> 50
Met Glu Tyr Ser Gly Ala Asp Pro Thr Phe Val Ala Lys Thr Ser Ala
  1             5             10             15
Leu Ala Val Thr His Pro Phe Cys Arg Ile Met Lys Arg Asp Gly Asn
    20             25             30

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Cys	Gly	Trp	Arg	Ala	Ala	Ala	Phe	Gly	Tyr	Phe	Glu	Ser	Leu	Phe	Asn
	35						40				45				
Leu	His	Asn	Leu	Ile	His	Ala	Gln	Ser	Glu	Leu	Val	Arg	Ile	Lys	Gly
	50					55				60					
Leu	Asn	Ser	Leu	Leu	Asp	Gln	Val	Gly	His	Gln	Glu	His	Leu	Tyr	Glu
65					70					75					80
Ile	Phe	Val	Asp	Ala	Thr	Glu	Ser	Val	Phe	Glu	Gln	Val	Cys	Glu	Ala
				85					90					95	
Ile	Gln	Ala	Gly	Val	Arg	Asp	Asp	Ser	Phe	Leu	Lys	Asp	Leu	Phe	Asn
			100					105					110		
Glu	Glu	Phe	Asn	Ser	Ser	Ala	Val	Ile	Thr	His	Phe	Arg	Leu	Leu	Thr
		115						120				125			
Ser	Ala	Trp	Met	Lys	Leu	Asn	Pro	His	Arg	Tyr	Gln	Ala	Phe	Leu	Pro
	130					135					140				
Leu	Pro	Leu	Asp	Gln	Tyr	Cys	Thr	Thr	Arg	Ile	Glu	Thr	Val	Lys	Thr
145					150					155					160
Glu	Ile	Asp	Glu	Val	Gly	Leu	Gln	Ala	Leu	Val	Asp	Gly	Val	Ile	Glu
				165					170					175	
Pro	Ser	Gly	Val	Ala	Val	Glu	Ile	Leu	Tyr	Leu	Asp	Arg	Ser	Gln	Gly
		180						185					190		
Glu	Ala	Val	Thr	Pro	His	Leu	Leu	Thr	Pro	Ser	Arg	Pro	Ser	Ala	Ser
		195					200					205			
Thr	Ile	Arg	Leu	Leu	Tyr	Arg	Pro	Gly	His	Tyr	Asp	Ile	Ala	Tyr	Gln
	210					215					220				
Ala	Glu	Pro	Thr	Val	Thr	Met	Glu	Pro	Ile	Val	Asn	Tyr	Gln	Tyr	Gly
225					230					235					240
Met	Thr	Thr	Asn	Tyr	Ser	Pro	Trp	Asp	Gln	Gly	Ala	Leu	Ser	Phe	Asp
				245					250					255	
Val	Asn	Ser	Ser	Leu	Met	Ser	Ile	Pro	Asn	Leu	Met	Met	Asp	Pro	Ser
			260					265					270		
Phe	Ala	Leu	Ser	Pro	Ser	Pro	Met	Thr	Pro	Ala	Pro	Ser	Pro	Tyr	Arg
		275					280					285			
Val	Ser	Pro	Pro	Gln	Glu	Val	Phe	Gln	Pro	Pro	Met	His	Thr	Pro	Pro
	290					295					300				
Pro	Pro	Val	Pro	Val	Ala	Ser	Pro	Pro	Pro	Pro	Arg	Met	Ser	Ala	Pro
305					310					315					320
Pro	Pro	Met	Thr	Ser	Leu	Pro	Asn	Arg	Ser	Ser	Asp	Gly	Pro	Gln	Ile
				325					330					335	
Arg	Leu	Asn	Pro	Leu	Val	Met	Lys	Gln	Asn	Leu	Ser	His	Ser	Leu	Pro
			340					345					350		
Val	Thr	Thr	Pro	Phe	Lys	Asn	Ser	Pro	Tyr	Asn	Gln	Ala	His	Phe	Gln
		355					360					365			
Asn	Gln	Asp	Phe	Glu	Pro	Ile	His	Trp	Glu	Pro	Ser	Asp	Ser	Arg	Lys
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<210> 51

<211> 2388

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 51

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ctgcaccatc aacacatcct agccaaccga tggcagcaga agaagctccg tcgacttcag 300
tccctggggc ccaaccagct ggttggtccc cgtcggggaa gaagctatct caagtcccag 360
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gaccgctctg cagcccagcc tcaagcagct ggccaaggt ggcgacctc catggaacac 720
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ctgatggaca agctcgtggg caacatgccg ggcgaccctg gcttgaatgg ggcaggcccc 2340
gatcacgcca catccgcgta ccctgagaac agcacggttg aggcggtt 2388

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<210> 52

<211> 796

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 52

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Ala Leu Glu Ser Val Gly Ala His Thr Asp Arg Ala Leu Gln Asn Thr
          20          25          30
Ser Gly Asn Val Gln Ser Tyr Ser Asp Asn Leu Ala Pro Asn Asp Thr
          35          40          45
Thr Gly Arg Asp Ser Gly His Leu Gln Pro Tyr Ala Pro Lys Tyr Pro
          50          55          60
Pro Pro Leu Pro Ile Pro Ala His Pro Val Pro Ser Ala Ala Ala Ser

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65					70				75				80
Leu	His	His	Gln	His	Ile	Leu	Ala	Asn	Arg	Trp	Gln	Gln	Lys
				85					90				Lys
Arg	Arg	Leu	Gln	Ser	Leu	Gly	Pro	Asn	Gln	Leu	Val	Gly	Pro
				100				105					Arg
Gly	Arg	Ser	Tyr	Leu	Lys	Ser	Gln	Lys	Tyr	Leu	Glu	Tyr	Arg
		115					120					125	Ala
Pro	Arg	Arg	Asp	Thr	Gly	Lys	Asp	Gly	Glu	Pro	Val	Trp	Ser
		130					135				140		Asp
Leu	Glu	Asp	Ala	Phe	Gln	Gln	Ala	Leu	Glu	Ala	Asn	Pro	Pro
145					150				155				Met
Arg	Arg	Lys	Trp	Ser	Glu	Arg	Gly	Lys	Ser	Tyr	Gly	Arg	Asn
				165					170				Glu
Ile	Ala	Glu	Phe	Ile	Tyr	Lys	Ala	Thr	Gly	Lys	Arg	Arg	Thr
			180					185					Arg
Gln	Val	Ser	Ser	His	Leu	Gln	Val	Leu	Asp	Ser	Phe	Leu	Lys
		195					200					205	Gly
Pro	Asp	Trp	Glu	Arg	Leu	Val	Arg	Glu	Gln	Pro	Thr	Asp	Arg
		210					215				220		Ser
Ala	Gln	Pro	Gln	Ala	Ala	Gly	Pro	Arg	Trp	Arg	Thr	Ser	Met
225					230					235			Glu
Pro	Leu	Ser	Ser	His	Tyr	Asn	His	Leu	His	Ala	Pro	Tyr	His
				245					250				Asp
Leu	Arg	Pro	Val	Gln	Pro	Tyr	Val	Gly	Glu	Leu	Pro	Pro	Pro
			260					265					Ser
Ala	Pro	Asn	Pro	Asn	Val	His	Asp	Ala	Asn	Ile	Asn	Thr	Val
		275					280					285	Gln
Leu	Asn	Phe	Asp	Met	Trp	Val	Ser	Ala	Pro	Asn	Gln	Pro	Asp
		290					295				300		Arg
Glu	Asn	Ala	Phe	His	Val	Tyr	Thr	Arg	Leu	Gln	Gly	Asp	Gln
305					310					315			Arg
Pro	Val	Ala	Pro	Ser	Met	Pro	Leu	Glu	Asn	Ile	Val	Gly	Trp
					325				330				Arg
Tyr	Phe	Pro	Tyr	Leu	Asn	Ser	Leu	Met	Ala	Asp	Pro	Thr	Ala
			340					345					Ser
Asn	Cys	Glu	Ile	Ile	Leu	Leu	Glu	Ala	Asn	Leu	Glu	Leu	Met
		355					360					365	Asp
Phe	Pro	Pro	Ser	Gly	Ser	Arg	Leu	Gly	Ile	Gln	Leu	Glu	Leu
		370				375					380		Asp
Ala	His	Ser	Ala	Val	Gly	Asp	Ala	Pro	Val	Ser	Gln	Met	Asp
385					390					395			Asn
Ser	Cys	Ser	Thr	Tyr	Met	Tyr	Glu	Glu	Ser	Gln	Lys	Ile	Leu
				405					410				Glu
Asn	His	Ser	Leu	Ser	Lys	Pro	Ala	Ser	Thr	Lys	Val	Lys	Pro
			420					425					Pro
Glu	Ser	Leu	Trp	Trp	Ala	Lys	Leu	Phe	Thr	Gln	Leu	Thr	Gln
		435					440					445	Glu
Gln	Met	Ala	Glu	Lys	Ala	Gly	Gln	His	His	Ala	Ala	Asp	Glu
		450				455					460		His
Arg	His	Phe	Phe	Arg	Thr	Met	Ser	Ala	Val	Gln	Glu	Ile	Arg
465					470					475			Ala
Ser	Pro	Asn	Ser	Arg	Arg	Leu	Ser	Ser	His	Tyr	Gly	Gly	Ser
				485					490				Ser
Asp	Glu	Ser	Lys	Arg	Val	Ala	Ile	Leu	Leu	Trp	Lys	Phe	Arg
			500					505				510	Gln
Arg	Pro	Gly	Glu	Val	Gly	Thr	Thr	Thr	Trp	Arg	Arg	Leu	Phe
		515					520					525	Pro

Pro Asp Arg Thr Ser Thr Asn Ser Pro Arg Pro Ala Thr Gly Ile Asp
 530 535 540
 Leu Pro Pro Leu Ser Leu Asp Ser Ile Leu Leu Asn Lys Pro Ala Pro
 545 550 555 560
 Asn Val Tyr Gln Ala Pro Pro Pro Gln Pro His Glu Leu Met His His
 565 570 575
 His Gly Ala Ser Gln Pro Pro Trp Gln Met Tyr Pro Pro Pro His Asp
 580 585 590
 His Met Tyr Pro Thr Gly Ser Phe Asp Leu Leu Asn Ser Ile Ser Lys
 595 600 605
 Pro Glu Asp Gly Leu Gly Asp Lys Thr Ala Val Ser Ser Val Ile Asp
 610 615 620
 Pro Phe Pro Asn Met Gln Gln His Glu Thr Ser Gln Pro Pro Asn Leu
 625 630 635 640
 Asn Gly Ser Asn Gly Gly Pro Ile Met Leu Asn Val Pro Asp Met Ser
 645 650 655
 Leu Ser His His Asn Leu Gly Gly Tyr Thr Met Gly His Glu Ser His
 660 665 670
 His Tyr Val Pro Pro Pro Gln Gln His Gly Val His Val Pro Asp Asn
 675 680 685
 Asn Ser Val Leu Asn Asn Ile Phe Ala Ser Gly Pro Gln Ser Phe Glu
 690 695 700
 Glu Leu Gly His Asn Ser His Ala Ala Trp Ser Gly Pro Ser Thr Thr
 705 710 715 720
 Leu Pro Ser Asp Val Gly Ser Asn Ser Tyr Gly His Leu Ser Tyr Gln
 725 730 735
 Ser Asp Gln His Pro Pro Ala Thr Arg Glu Pro His Gln Ser Asn Gly
 740 745 750
 Phe Glu Gly Leu Met Gly Thr Asp Leu Met Asp Lys Leu Val Gly Asn
 755 760 765
 Met Pro Gly Asp Pro Gly Leu Asn Gly Ala Gly Pro Asp His Ala Thr
 770 775 780
 Ser Ala Tyr Pro Glu Asn Ser Thr Val Glu Ala Val
 785 790 795

<210> 53

<211> 1431

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 53

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 ccttcgcttg gtcacacctg ttctcgcggc aatccgaata ccaacatcaa cccttttaca 180
 ctatccggcg gaattgcaaa tggatatggc gtagccggct tcccgggagc tgggtcaggt 240
 gatggcgggc gcaccgggtc ggctagtcac gcggcacaga tgggattcgc gcgcggtgcg 300
 caaatgcaac aacagcaact acaccagggt cacgacggtc ggtttagcgt cgaagcaaaag 360
 ggcggtgcag tgaagtcaag aattagagat gtctggaagc acaacctggc ccatgagatg 420
 gcggtgctga ggcagttggc cgacaagtac ccttacatca gcatggacac cgagttccct 480
 ggtattgttg ctcggccgat agggctcttt tcgaacaaaag ccgattacca ttatcagacc 540
 ctccgatgca atgttgatct tctgaagatg atacaactag gcatcacgtt attcaatgac 600
 gaaggagagg tccccccagc ctcaggcact gatgccaatg gacaagcgta tgggtgtgcc 660
 gctccctgca catggcagtt caacttccga ttttcacttg aaggcgacat gtacgcccag 720

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gttcactggg tgtctttcca ctccgggtac gactttgggt acttgatgaa gatcatgctc 900
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gcctacaaca tggctcagca aacgcccac cttaatggcg cgaccattta ctcgggcggc 1320
acccccagca ctcccataac tgggtctcac ggggctggcg cccacacacc tcagcactac 1380
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<210> 54

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 54

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20     25     30
Gln Ser Gly Asn Thr Leu Pro Pro Pro Ser Leu Gly His Pro Gly Phe
35     40     45
Ala Gly Asn Pro Asn Thr Asn Ile Asn Pro Phe Thr Leu Ser Gly Gly
50     55     60
Ile Ala Asn Gly Met Ala Val Ala Gly Phe Pro Gly Ala Gly Ala Gly
65     70     75     80
Asp Gly Gly Gly Thr Gly Leu Ala Ser His Ala Ala Gln Met Gly Phe
85     90     95
Ala Arg Gly Ala Gln Met Gln Gln Gln Gln Leu His Gln Gly His Asp
100    105    110
Gly Arg Leu Ala Leu Glu Ala Lys Gly Gly Ala Val Lys Ser Arg Ile
115    120    125
Arg Asp Val Trp Lys His Asn Leu Ala His Glu Met Ala Val Leu Arg
130    135    140
Gln Leu Val Asp Lys Tyr Pro Tyr Ile Ser Met Asp Thr Glu Phe Pro
145    150    155    160
Gly Ile Val Ala Arg Pro Ile Gly Ser Phe Ser Asn Lys Ala Asp Tyr
165    170    175
His Tyr Gln Thr Leu Arg Cys Asn Val Asp Leu Leu Lys Met Ile Gln
180    185    190
Leu Gly Ile Thr Leu Phe Asn Asp Glu Gly Glu Val Pro Pro Ala Ser
195    200    205
Gly Thr Asp Ala Asn Gly Gln Ala Tyr Gly Val Pro Ala Pro Cys Thr
210    215    220
Trp Gln Phe Asn Phe Arg Phe Ser Leu Glu Gly Asp Met Tyr Ala Gln
225    230    235    240
Glu Ser Thr Ala Met Leu Ala Lys Ser Gly Ile Asp Phe Ala Met His
245    250    255
Glu Lys Asn Gly Ile Asp Pro Phe Glu Phe Gly Ala Leu Leu Ile Ser
260    265    270
Ser Gly Leu Val Leu Leu Asp Asp Val His Trp Val Ser Phe His Ser

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275	280	285
Gly Tyr Asp Phe Gly Tyr	Leu Met Lys Ile Met	Leu Cys Ser Gln Leu
290	295	300
Pro Glu Asn Glu Glu Glu	Phe His Lys Leu Leu	Thr Ile Phe Phe Pro
305	310	315
Ser Leu Tyr Asp Ile Lys	Tyr Leu Met Lys His	Ala Gly Arg Asn Gln
325	330	335
Ala Val Asn Gly Ser Pro	Leu Ser Gln Ala Ala	Ala Gln Ile Leu Thr
340	345	350
Asn Leu Gly Gln Lys Ser	Gly Leu Gln Asp Ile	Ala Asp Glu Leu Gly
355	360	365
Val Lys Arg Val Gly Ile	Ala His Gln Ala Gly	Ser Asp Ser Leu Val
370	375	380
Thr Gly Glu Ile Tyr Trp	Lys Thr Arg Gln Leu	Ile Phe Gly Gly Ala
385	390	395
Ile Asp Asp Ser Lys Tyr	Ser Gly Gln Ile Trp	Gly Leu Asn Gly Gln
405	410	415
Met Pro Ala Val Ala Tyr	Asn Met Ala Gln Gln	Thr Pro Asn Leu Asn
420	425	430
Gly Ala Thr Ile Tyr Ser	Gly Gly Thr Pro Ser	Thr Pro Asn Thr Gly
435	440	445
Ser His Gly Ala Gly Ala	His Thr Pro Gln His	Tyr Gly Ala Gly Tyr
450	455	460
Asn Ala Pro Thr Pro Gly	Ala Tyr Gln Met Gly	Arg Val
465	470	475

<210> 55

<211> 1146

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 55

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caaaatgctg ctgggggtatt cgcaagcccc actagcacac actactctgt atctcgtgat 240
gagggtacct taagcgcggc cgaggcggag atgcggagga gaacgtggca cccttcgtca 300
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<210> 56
 <211> 382
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 56

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			20					25					30		
Val	Pro	Thr	Ser	Ser	Asn	Pro	Phe	Leu	Ala	Gln	His	Gly	Asn	Ala	Tyr
			35				40					45			
Pro	Pro	Gly	Tyr	His	Asn	Pro	Val	Gly	Ala	Pro	Tyr	Gln	Asn	Ala	Ala
			50			55					60				
Gly	Val	Phe	Ala	Ser	Pro	Thr	Ser	Thr	His	Tyr	Ser	Val	Ser	Arg	Asp
65					70					75					80
Glu	Gly	Thr	Leu	Ser	Ala	Ala	Glu	Ala	Glu	Met	Arg	Arg	Arg	Thr	Trp
			85						90					95	
His	Pro	Ser	Ser	Tyr	Thr	Gly	Phe	Pro	Arg	Pro	Gly	Thr	Ser	Gly	Leu
			100					105					110		
Asn	Gln	Tyr	His	Thr	Pro	Asp	Asn	Val	Pro	Ala	Ser	Phe	Gly	Ala	Asn
			115				120					125			
Gly	Ser	Thr	Glu	His	Pro	Pro	Arg	Leu	Pro	Gly	Ile	Glu	Ser	Phe	Asp
			130			135					140				
Lys	Val	Val	Gln	Arg	Pro	Met	Thr	Pro	Pro	Thr	Arg	Lys	Thr	Ser	Pro
145					150					155					160
Met	Gln	Leu	Asp	Gly	Gln	His	Arg	Pro	Pro	Pro	Asn	Pro	Gly	Phe	Gly
			165						170					175	
Ser	Gly	Phe	Asn	Tyr	Thr	Gln	Pro	Ala	His	Arg	Pro	Pro	Pro	Pro	Ile
			180					185					190		
Ser	Gly	Pro	Gly	His	Arg	Arg	Gly	His	Val	Ser	Trp	Asp	Met	Ser	Leu
			195				200					205			
His	His	Asn	Leu	Thr	Gly	Leu	Asp	Ile	Arg	Asp	Arg	Arg	Pro	Ser	Thr
			210			215					220				
Ala	Ser	Ala	Ser	Gln	Trp	Ser	Gln	Gln	Thr	Leu	Ala	Glu	Leu	Gln	Asn
225					230					235					240
Val	Ser	Ser	Arg	Pro	Ser	Ser	Ser	Tyr	Gln	Pro	Ala	Phe	Gly	Pro	Thr
			245						250					255	
Ala	Glu	Arg	Ser	Pro	Glu	Glu	Tyr	Arg	Gly	His	Arg	Pro	Ser	Leu	Ser
			260					265					270		
Thr	Gly	Ser	Arg	Thr	Arg	Thr	Ser	Pro	Glu	Asp	Ser	Ser	Ser	Ser	Glu
			275				280					285			
Gly	Val	His	Thr	Pro	Ser	Thr	Ala	Ser	Leu	Glu	Tyr	His	Pro	Ala	Ile
			290			295					300				
Val	His	Ser	Ser	Gly	Tyr	Ile	Glu	Ser	Asp	Asp	Ser	Ser	Leu	Pro	Ser
305					310					315					320
Asp	His	Pro	Gln	Pro	Ile	Cys	Gly	Arg	Gln	Ser	Ser	His	Ala	Asp	Gly
			325						330					335	
Tyr	Glu	Pro	His	Asn	Asp	Arg	Glu	Pro	Arg	Pro	Asp	Val	Phe	Pro	Asp
			340					345					350		
Ser	Pro	Ala	Arg	Asn	Ser	Gly	Met	Gly	Arg	Leu	Glu	Ala	Leu	Val	Ala
			355				360					365			
Val	Ala	Thr	Ser	Glu	Asn	Lys	Gly	Ala	Ala	Lys	Leu	Phe	Leu		
			370			375					380				

<210> 57
 <211> 909
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 57
 aagacgatga gcgtgacggt tttgggcggtg acccaccatt tgggtctcata ctacagtgtg 60
 gaggacgtga tgcgcggcat cctcaaccca cctcgatgg tggattccct acgctttatc 120
 cgaccccgca ccgaactcac ccagaaacaa agcttccggt ccccgatcga cgagctcgag 180
 gccaacgccc tggaaaacca ggagccctcc cacgctgctc tatacggata tcgcccgcag 240
 atgatggccc ctcccacgta cgccatgcca accccttcaa acgacttcta catgcacccc 300
 agtccctacg ccgccacaca tccccgcgag caaggcccga tccaggata ctcgatgggc 360
 gcccgatgg cagcccaaac cgcgccaaac ccatacctgc caagcccagg ccaaaccgcc 420
 atcccaccga agcaggaaga ctaccacgca ttccgcgcag ggccttatgg cggcagcatg 480
 gactccatga gcgcacacag catggcctcc atcccgggca gcatcaacgc ggggctgtcc 540
 agtccactca acgaacgaaa cagatccacc tcggatcaca gcccttccgc ttaccgcaat 600
 tcttccatct cttcgcgcag ccaggccact gacgctactt ccccatgga tccatcaaca 660
 ccggccacct actccgcgag cagcttcagc atgtccggtc aactggagaa cccacatcca 720
 gcactcgatc gcaacatgcc tggctctggat gctagcggtc gtcgcgagtc aaatcctatt 780
 catccgtcct actaacctgc ggatcgctcc cagtactatg taccgcgcgc ttacgctgcc 840
 acgcaaccta tgtcgacatg gacgactacg gcggcgacgc aaccacagat ggcgcaacct 900
 caaatctaa 909

<210> 58
 <211> 302
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 58
 Lys Thr Met Ser Val Thr Val Leu Gly Val Thr His His Leu Val Ser
 1 5 10 15
 Tyr Tyr Ser Val Glu Asp Val Met Arg Gly Ile Leu Asn Pro Pro Ser
 20 25 30
 Met Val Asp Ser Leu Arg Phe Ile Arg Pro Arg Thr Glu Leu Thr Gln
 35 40 45
 Lys Gln Ser Phe Arg Ser Pro Ile Asp Glu Leu Glu Ala Asn Ala Val
 50 55 60
 Glu Asn Gln Glu Pro Ser His Ala Ala Leu Tyr Gly Tyr Arg Pro Gln
 65 70 75 80
 Met Met Ala Pro Pro Thr Tyr Ala Met Pro Thr Pro Ser Asn Asp Phe
 85 90 95
 Tyr Met His Pro Ser Pro Tyr Ala Ala Thr His Pro Pro Gln Gln Gly
 100 105 110
 Pro Ile Gln Gly Tyr Ser Met Gly Ala Pro Met Ala Ala Gln Thr Ala
 115 120 125
 Pro Asn Pro Tyr Leu Pro Ser Pro Gly Gln Thr Ala Ile Pro Pro Lys
 130 135 140
 Gln Glu Asp Tyr His Ala Phe Arg Ala Gly Pro Tyr Gly Gly Ser Met
 145 150 155 160

Asp Ser Met Ser Ala His Ser Met Ala Ser Ile Pro Gly Ser Ile Asn
 165 170 175
 Ala Gly Leu Ser Ser Ser Leu Asn Glu Arg Asn Arg Ser Thr Ser Asp
 180 185 190
 His Ser Pro Ser Ala Tyr Arg Asn Ser Ser Ile Ser Ser Arg Ser Gln
 195 200 205
 Ala Thr Asp Ala Thr Ser Pro Met Asp Pro Ser Thr Pro Ala Thr Tyr
 210 215 220
 Ser Arg Gly Ser Phe Ser Met Ser Gly Gln Leu Glu Asn Pro His Pro
 225 230 235 240
 Ala Leu Asp Arg Asn Met Pro Gly Leu Asp Ala Ser Val Arg Arg Glu
 245 250 255
 Ser Asn Pro Ile His Pro Ser Tyr Tyr Thr Ala Asp Arg Ser Gln Tyr
 260 265 270
 Tyr Val Pro Ala Pro Tyr Ala Ala Thr Gln Pro Met Ser Thr Trp Thr
 275 280 285
 Thr Thr Ala Ala Thr Gln Pro Gln Met Ala Gln Pro Gln Ile
 290 295 300

<210> 59
 <211> 918
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 59
 atggtctccag gcagtgggcg cgactttaac tgctcatggg agcattgtgg aaagtctttc 60
 aatcgcaagt cggatctctg tcgccattat cgcattccata ccaatgagcg cccgtatcat 120
 tgcaccgtaa aggactgcaa taagagcttc attcagcgga gtgccttgac cgtacactcg 180
 aggaccaca ctggcgaaaa gccccatggt tgtgaccatg aaggctgtca gaaggcattc 240
 tccgactcat cgagtctagc tcgccatcgc cgaatccaca ccgggaagcg gccatacata 300
 tgccacgagc ctacatgcga acggagtttt tgctcgcaaga ccaccctcac caaacaccaa 360
 caccgctccc accctccagg gagcttgacc cgaccatcct cagaagatgg gacctccgag 420
 cattcttacc accaaacacc cgtatcagtc tcggtcccga ctgagcagta catgctcgcc 480
 cagcaacctt tttaccgca atcggcgaca ccaagtcatg agttttactc gcccacaaagt 540
 gtgccgatgg gcaccgtgcc gggttcacgaa gctgcccctc cgatcgtggc ccagactgtc 600
 cccggaacct cgccggtaaa catgccacac gctcaacagc cgcagccgca cccgcaacac 660
 cagcgcatc cacaacagca gcagcagcag cagcagcagc agcatcaaca atacttacia 720
 atgatgaac agcgttacga cagtccacgg gcgaactacc tcccagaaca ataccaacat 780
 ccattctttc aaggccacca actgcctccc gaacagccaa tgatgggttc ataccacca 840
 aactatgcgt ataaaccccc cggtcccggt ctcttgaacc aagcggaggg gactgactgg 900
 ggctttctgg gagtaggc 918

<210> 60
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 60
 Met Ala Pro Gly Ser Gly Arg Asp Phe Asn Cys Ser Trp Glu His Cys
 1 5 10 15

Gly Lys Ser Phe Asn Arg Lys Ser Asp Leu Cys Arg His Tyr Arg Ile
 20 25 30
 His Thr Asn Glu Arg Pro Tyr His Cys Thr Val Lys Asp Cys Asn Lys
 35 40 45
 Ser Phe Ile Gln Arg Ser Ala Leu Thr Val His Ser Arg Thr His Thr
 50 55 60
 Gly Glu Lys Pro His Val Cys Asp His Glu Gly Cys Gln Lys Ala Phe
 65 70 75 80
 Ser Asp Ser Ser Ser Leu Ala Arg His Arg Arg Ile His Thr Gly Lys
 85 90 95
 Arg Pro Tyr Ile Cys His Glu Pro Thr Cys Glu Arg Ser Phe Cys Arg
 100 105 110
 Lys Thr Thr Leu Thr Lys His Gln His Arg Ser His Pro Pro Gly Ser
 115 120 125
 Leu Thr Arg Pro Ser Ser Glu Asp Gly Thr Ser Glu His Ser Tyr His
 130 135 140
 Gln Thr Pro Val Ser Val Ser Val Pro Thr Glu Gln Tyr Met Leu Ala
 145 150 155 160
 Gln Gln Pro Phe Tyr Pro Gln Ser Ala Thr Pro Ser His Glu Phe Tyr
 165 170 175
 Ser Pro Gln Ser Val Pro Met Gly Thr Val Pro Val His Glu Ala Ala
 180 185 190
 Pro Pro Ile Val Ala Gln Thr Val Pro Gly Thr Ser Pro Val Asn Met
 195 200 205
 Pro His Ala Gln Gln Pro Gln Pro His Pro Gln His His Ala His Pro
 210 215 220
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Gln Gln Tyr Leu Gln
 225 230 235 240
 Met Met Gln Gln Arg Tyr Asp Ser Pro Arg Ala Asn Tyr Leu Pro Glu
 245 250 255
 Gln Tyr Gln His Pro Ser Phe Gln Gly His Gln Leu Pro Pro Glu Gln
 260 265 270
 Pro Met Met Val Ser Tyr His Pro Asn Tyr Ala Tyr Lys Pro Pro Gly
 275 280 285
 Ser Arg Leu Leu Asn Gln Ala Glu Gly Thr Asp Trp Gly Phe Leu Gly
 290 295 300
 Val Gly
 305

<210> 61

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 61

atggataccc attcggatac cgacttgagt catcctcgaa tgcgcggagc tattgaaactg 60
 cccccgctcc gcgatcattt caagcaggaa tctcttcgcg cgtttacgcc tcgtcctcgc 120
 gagcttcttc catccatcct caatcactcc cgcgccggtc gtcctaccac attgccgcca 180
 atccagcgga gagacaaatt ttcccgcccg cgcaaacttt ccatcactca atctgcgcgg 240
 aaatccaggc aggatcgccc taaatcaaag gaattcgggc ggcgaccaag tctcggtgac 300
 cgcaaagccc ttctggcaga gccgcaaacc gcggcctggg cgcaaggcaa gcgctgggag 360
 gatctgattg aagccgcgac atcagcaacc gaagtagacg atgagccgta ttcagaggct 420
 ggtcggtctc caacgattgc cccactactt tccaacgtga cgtctgcccc ctctgggggtg 480

```

aaaaatcggg cctcgctacc acccgctttc caatcctcgg gattgcctcc tatctcttca 540
catcggccat tcccacctca ttcatacgcc gcctcgccctt tgcacaagtc attgacccca 600
ccaccatacg agaaccaccg cagcgtgag agcgacttgg aaccattccc gtctattgaa 660
tcatcgctcg attccatgtc ttcggcatcc ggcagaaatt ttgcgtcatc ggtttcggga 720
gtcgcgccgt ccataaaactc tgattccagc ccagttatga atcttatccc gcccatctcg 780
cagcgccagc accaccgatt ctccaatcct actccagcgt ctttccgcaa caaagagggt 840
caggtgtttt gtgctcagtg caaacgacct tcggcactga atgagtgcta tgcctgtacg 900
gagtgcattc gtggagtctg ccgcgactgc gtgagcatgt tcatttcaag tccgcctact 960
tcattccgaa cccaggggaa cgggtcgtta aataccgtcc tgtcacaagg accaacaagt 1020
taccctggtc ctcaagggtg tccacgatgt cgaacagttg gaggc aaatg gaaggcattc 1080
caaatcgaca tcaag 1095

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<210> 62

<211> 365

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 62

```

Met Asp Thr His Ser Asp Thr Asp Leu Ser His Pro Arg Met Arg Gly
1      5      10      15
Ala Ile Glu Leu Pro Pro Leu Arg Asp His Phe Lys Gln Glu Ser Leu
20     25     30
Pro Pro Phe Thr Pro Arg Pro Arg Glu Leu Leu Pro Ser Ile Leu Asn
35     40     45
His Ser Pro Pro Gly Arg Ser Ser Thr Leu Pro Pro Ile Gln Arg Arg
50     55     60
Asp Lys Phe Ser Arg Pro Arg Lys Ser Ser Ile Thr Gln Ser Ala Arg
65     70     75     80
Lys Ser Arg Gln Asp Arg Pro Lys Ser Lys Glu Phe Gly Arg Arg Pro
85     90     95
Ser Leu Gly Asp Arg Lys Ala Leu Ser Ala Glu Pro Gln Thr Ala Ala
100    105    110
Trp Ala Gln Gly Lys Arg Trp Glu Asp Leu Ile Glu Ala Ala Thr Ser
115    120    125
Ala Thr Glu Val Asp Asp Glu Pro Tyr Ser Glu Ala Gly Arg Ser Pro
130    135    140
Thr Ile Ala Pro Leu Leu Ser Asn Val Thr Ser Ala Pro Ser Gly Val
145    150    155    160
Lys Asn Arg Ser Ser Leu Pro Pro Ala Phe Gln Ser Ser Gly Leu Pro
165    170    175
Pro Ile Ser Ser His Arg Pro Phe Pro Pro His Ser Tyr Ala Ala Ser
180    185    190
Pro Leu His Lys Ser Leu Thr Pro Pro Pro Tyr Glu Asn His Arg Ser
195    200    205
Arg Glu Ser Asp Leu Glu Pro Phe Pro Ser Ile Glu Ser Ser Leu Asp
210    215    220
Ser Met Ser Ser Ala Ser Gly Arg Asn Phe Ala Ser Ser Val Ser Gly
225    230    235    240
Val Ala Pro Ser Ile Asn Ser Asp Ser Ser Pro Val Met Asn Leu Ile
245    250    255
Pro Pro Ile Ser Gln Arg Gln His His Arg Phe Ser Asn Pro Thr Pro
260    265    270
Ala Ser Phe Arg Asn Lys Glu Val Gln Val Phe Cys Ala Gln Cys Lys
275    280    285

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Arg Pro Ser Ala Leu Asn Glu Cys Tyr Ala Cys Thr Glu Cys Ile Cys
 290                               295                 300
Gly Val Cys Arg Asp Cys Val Ser Met Phe Ile Ser Ser Pro Pro Thr
305                               310                 315                 320
Ser Phe Arg Thr Pro Gly Asn Gly Ser Leu Asn Thr Val Leu Ser Gln
                               325                 330                 335
Gly Pro Thr Ser Tyr Pro Gly Pro Gln Gly Cys Pro Arg Cys Arg Thr
                               340                 345                 350
Val Gly Gly Lys Trp Lys Ala Phe Gln Ile Asp Ile Lys
      355                               360                 365

```

<210> 63
 <211> 1197
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 63
atgaagagcg aatcaggtgg ctcggaacaac cctgtcaatg cataccctcc tcatggtcct 60
ccgcccattgc agatggatgc tggacttgcg gattccttct attatgcaca gccacgggt 120
tcaacccctc gaaacatggc ctatgccctt gcgggatacg ctggcgatcc ccagatgcag 180
caggaacctg tcccgcaggg aagagcaggg gttgaaccac cgccaaagac tttccactgc 240
tcaacctgca acaagggctt cgcacggcgc agtgacctg ctcgacatga gcgtattcac 300
accggagtta gaccccatgc atgcgagtgg ccggggtgtg gaaagcagtt cattcaacgc 360
tcggctttaa cagtgcactc ccgtgtacac actggagaga agcctcatat gtgtgagaga 420
tgtggcaagc ccttttagcga ctgcgtcctcg ctggccagac atcgtcgcat tcaactccggc 480
aagcgaccct acaaatgccc gtacgccaac tgtcagaaga ccttcacgcg ccgtacgacg 540
ttgacacgcc accaaaacca ccacactggg accatcgaag aagccgctgc tgaaaccgag 600
gcccatttgc ggcaaaataa ggatcggtga cgtcctggtg aaggaatgtt ctccgagcac 660
gcttccatcc actctacacc gtcaccgcg cagcatccat ccatgtcacc tggtagcgag 720
cttccccgcg tgaatatgca tcgctcagct ggcgactact acatgggcac cggtcctatc 780
ccgctcatg tgcgtgggga tttcccccaa ggcagccctc gggttcccc gactgcgacc 840
tctccttcgc tgtccagcta tggcagtgcg cccacacccc ggccatccat gacctcgcat 900
ccctacgctc cgcctcagcc tcttgaaccc ccggccaaca gtgatcaccg tcccaatagt 960
gtgaacggca gtccacacat gactagtctc ggatgggcct cgccgtctca cggtagcatg 1020
ccgtcgcccg gatcgcccaa cgacttcact taccgcgagc ccactggccc tgcgtacccg 1080
acatcgatgc cgccacacat gtacttcccc aattctacta ttcgtcggcc taccagcacc 1140
gagccggaga actacgaaat gaagcctcga ggtgaccact catggtccac tgctgta 1197

```

<210> 64
 <211> 399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 64
Met Lys Ser Glu Ser Gly Gly Ser Asp Asn Pro Val Asn Ala Tyr Pro
 1                               5                 10                 15
Pro His Gly Pro Pro Pro Met Gln Met Asp Ala Gly Leu Ala Asp Ser
      20                               25                 30
Phe Tyr Tyr Ala Gln Pro Thr Gly Ser Thr Pro Arg Asn Met Ala Tyr
      35                               40                 45

```

Ala	Pro	Ala	Gly	Tyr	Ala	Gly	Asp	Pro	Gln	Met	Gln	Gln	Glu	Pro	Val
50						55				60					
Pro	Gln	Gly	Arg	Ala	Gly	Val	Glu	Pro	Pro	Pro	Lys	Thr	Phe	His	Cys
65					70					75					80
Ser	Thr	Cys	Asn	Lys	Gly	Phe	Ala	Arg	Arg	Ser	Asp	Leu	Ala	Arg	His
			85					90						95	
Glu	Arg	Ile	His	Thr	Gly	Val	Arg	Pro	His	Ala	Cys	Glu	Trp	Pro	Gly
			100					105					110		
Cys	Gly	Lys	Gln	Phe	Ile	Gln	Arg	Ser	Ala	Leu	Thr	Val	His	Ser	Arg
		115					120					125			
Val	His	Thr	Gly	Glu	Lys	Pro	His	Met	Cys	Glu	Arg	Cys	Gly	Lys	Pro
		130					135				140				
Phe	Ser	Asp	Ser	Ser	Ser	Leu	Ala	Arg	His	Arg	Arg	Ile	His	Ser	Gly
145					150					155					160
Lys	Arg	Pro	Tyr	Lys	Cys	Pro	Tyr	Ala	Asn	Cys	Gln	Lys	Thr	Phe	Thr
				165					170						175
Arg	Arg	Thr	Thr	Leu	Thr	Arg	His	Gln	Asn	His	His	Thr	Gly	Thr	Ile
			180					185					190		
Glu	Glu	Ala	Ala	Ala	Glu	Thr	Glu	Ala	Gln	Leu	Arg	Gln	Asn	Lys	Asp
		195					200					205			
Arg	Gly	Arg	Pro	Gly	Glu	Gly	Met	Phe	Ser	Glu	His	Ala	Ser	Ile	His
		210				215					220				
Ser	Thr	Pro	Ser	Pro	Ala	Gln	His	Pro	Ser	Met	Ser	Pro	Gly	Gly	Glu
225					230					235					240
Leu	Pro	Pro	Leu	Asn	Met	His	Arg	Ser	Ala	Gly	Asp	Tyr	Tyr	Met	Gly
				245					250					255	
Thr	Gly	Pro	Ile	Pro	Pro	His	Val	Arg	Gly	Asp	Phe	Pro	Gln	Gly	Ser
			260					265					270		
Pro	Arg	Ala	Ser	Pro	Thr	Ala	Thr	Ser	Pro	Ser	Leu	Ser	Ser	Tyr	Gly
		275					280					285			
Ser	Ala	Pro	His	Thr	Arg	Pro	Ser	Met	Thr	Ser	His	Pro	Tyr	Ala	Pro
		290				295					300				
Pro	Gln	Pro	Leu	Glu	Pro	Pro	Ala	Asn	Ser	Asp	His	Arg	Pro	Asn	Ser
305					310					315					320
Val	Asn	Gly	Ser	Pro	His	Met	Thr	Ser	Leu	Gly	Trp	Ala	Ser	Pro	Ser
				325					330					335	
His	Gly	Ser	Met	Pro	Ser	Pro	Gly	Ser	Ala	Asn	Asp	Phe	Thr	Tyr	Pro
			340					345					350		
Glu	Pro	Thr	Gly	Pro	Ala	Tyr	Pro	Thr	Ser	Met	Pro	Pro	His	Met	Tyr
		355					360					365			
Phe	Pro	Asn	Ser	Thr	Ile	Arg	Arg	Pro	Thr	Ser	Thr	Glu	Pro	Glu	Asn
		370				375					380				
Tyr	Glu	Met	Lys	Pro	Arg	Gly	Asp	His	Ser	Trp	Ser	Thr	Ala	Val	
385					390					395					

<210> 65

<211> 1098

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 65

atgtctaacg caaggcattg ggaacaagat aaagaggcaa ccgtgtacat cggaacacctt 60
gatgaacggg tctcgacag cctggtatgg gaattgatgc tgcaggttgg gcgcacgcgtt 120

```

aacgtccatc tgcctaaaga cggggtcacg cagttacacc aggggtatgg atttggtgag 180
ttcatcagcg aggaagatgc cgaatatgca tcgaagatca tgaacggaat ccgtctccat 240
ggcaagccta ttcgtgttaa caaggcatcg gctgataagc aaaaaactgt ggaaattggc 300
gctgagctgt ttgtgggtaa tcttgatcct atggttgccg agcaggttct ctttgatacg 360
ttcagccggt ttggcaatct tgtcaatccg cctaaaattg cccgtgatga caacaatctc 420
tctaagggat atggatttgt ttcttttgcc gatttcgaat cctcggaagc ggctatcgcc 480
aacatgaatg gccagtacct gatgaacaaa caggtttctg tacagtatgc atacaagaag 540
gatgggaaag gcgagagaca tgggtgatgaa gcagaacgaa tgctggcagc ccaggctcgc 600
aagcataatg cacagccacc cactcagcaa gtcgccgagt tccctggcac tggcccgggc 660
gtatcatcaa cgccggccat gtcgaatggc gacatctctc gacccttgag cacagccccg 720
tcacaaacac ccgatgtagg tatgaatcgg ggtgtgaccc cagccatggc tccagctatg 780
cctccagctt tgcctacca gagtgcgcct cctccaatgc cttaccagac cggtccccct 840
ccaaaccgac atgtcccacc tcccgtcctt tcaactaata cgccacctcc ggggctccca 900
gctcggcctc cgcttcccca agctggctac ggcgcccccac agaccttttt accacctgga 960
ttcaatggtg caggccaacc gcccttcac cccaggtgac cactcctccc tggggttggg 1020
ccgcccggat ttggacctcc atctggggcc ccttcattgc caccgggctt ccaacagccc 1080
ggatacggag gcagtcgg                                     1098

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<210> 66

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 66

```

Met Ser Asn Ala Arg His Trp Glu Gln Asp Lys Glu Ala Thr Val Tyr
 1           5           10           15
Ile Gly Asn Leu Asp Glu Arg Val Ser Asp Ser Leu Val Trp Glu Leu
      20           25           30
Met Leu Gln Val Gly Arg Ile Val Asn Val His Leu Pro Lys Asp Arg
      35           40           45
Val Thr Gln Leu His Gln Gly Tyr Gly Phe Val Glu Phe Ile Ser Glu
      50           55           60
Glu Asp Ala Glu Tyr Ala Ser Lys Ile Met Asn Gly Ile Arg Leu His
      65           70           75           80
Gly Lys Pro Ile Arg Val Asn Lys Ala Ser Ala Asp Lys Gln Lys Thr
      85           90           95
Val Glu Ile Gly Ala Glu Leu Phe Val Gly Asn Leu Asp Pro Met Val
      100          105          110
Ala Glu Gln Val Leu Phe Asp Thr Phe Ser Arg Phe Gly Asn Leu Val
      115          120          125
Asn Pro Pro Lys Ile Ala Arg Asp Asp Asn Asn Leu Ser Lys Gly Tyr
      130          135          140
Gly Phe Val Ser Phe Ala Asp Phe Glu Ser Ser Asp Ala Ala Ile Ala
      145          150          155          160
Asn Met Asn Gly Gln Tyr Leu Met Asn Lys Gln Val Ser Val Gln Tyr
      165          170          175
Ala Tyr Lys Lys Asp Gly Lys Gly Glu Arg His Gly Asp Glu Ala Glu
      180          185          190
Arg Met Leu Ala Ala Gln Ala Arg Lys His Asn Ala Gln Pro Pro Thr
      195          200          205
Gln Gln Ala Pro Gln Phe Pro Gly Thr Gly Pro Gly Val Ser Ser Thr
      210          215          220
Pro Ala Met Ser Asn Gly Asp Ile Ser Arg Pro Leu Ser Thr Ala Pro
      225          230          235          240

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Ser Gln Thr Pro Asp Val Gly Met Asn Arg Gly Val Thr Pro Ala Met
                245                250                255
Ala Pro Ala Met Pro Pro Ala Leu Pro Tyr Gln Ser Ala Pro Pro Pro
                260                265                270
Met Pro Tyr Gln Thr Val Pro Pro Pro Asn Arg His Val Pro Pro Pro
                275                280                285
Val Pro Ser Leu Asn Thr Pro Pro Pro Gly Leu Pro Ala Arg Pro Pro
                290                295                300
Pro Ser Gln Ala Gly Tyr Gly Gly Pro Gln Thr Phe Leu Pro Pro Gly
305                310                315                320
Phe Asn Gly Ala Gly Gln Pro Pro Phe Ile Pro Gln Ala Ala Pro Pro
                325                330                335
Pro Gly Phe Gly Pro Pro Gly Phe Gly Pro Pro Ser Gly Ala Pro Ser
                340                345                350
Leu Pro Pro Gly Phe Gln Gln Pro Gly Tyr Gly Gly Ser Arg
                355                360                365

```

<210> 67
 <211> 1077
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 67
atggttcttc tcaaaaagca tttgaaagat gtcaaccgtg aggatcagag gcaaatgccg 60
aggcaacggc tgccatctat tcaagaaata tttggggaga cttttctggc gattccttca 120
aatccatcat atgcaactgcc ttctcacacc agacatgccg ctccaccggc ttgcccggct 180
gtgtatgaaa ttgcccatc aatcgaaggg gctccgtcaa atgagcaagg tttattaccc 240
aaaatttcaa cagtggagag atctttgggc attatctctc ccgtcaatga gctccagcat 300
ccggaggtaa tacgcccga aaatccatcc ttctctcoga acggttggtc tcttaacgaa 360
agccgtcgtc tttcaaagca cccggacctc tctataacctc aaccgggttt attgtcatgc 420
gatcccatgg atttagcaca gccgtccttt gtcgaacctc caaatgtgtt tcatggattt 480
cccacagga aaataccaaa ctcgataccg cctcagccaa agcagttatg tctgccggaa 540
aaacgaacac cgagttctct tgatttcagt ctgtttttta aggtgatcga gacagtcagc 600
gcacagacct tggctttcgt gcggtatcac tccgcaatga gtcagtcaga caaccatcaa 660
agatccctcc ctggactatc tatcactgag ataaatggcc tcctcagtca ggagcagcaa 720
aagcaggatg tcttgattta tattagggat gaacttgtgc gcttcgacca ataccaagcc 780
ttagcgcagc agaataactcg ggcagccgca tgtatggcgg gtggggctga ccgaggtctt 840
tgttcatcag tcaactaaaca gagcaagacc cataaagtct ctaaacaaaa aagagaatgg 900
cacggggata gtgctcttcg ttgtcatagc tgcaaccgtt ctgaaacacc agaattggcg 960
cgtgggtccg acggcccccg aactctttgt aacgcctgtg gtttacatta tgcaaaattg 1020
tctcgacgaa cgggcaaatt tgtggcggtg gacgatattg gcatcagggg caaaaca 1077

```

<210> 68
 <211> 359
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 68
Met Val Leu Leu Lys Lys His Leu Lys Asp Val Asn Arg Glu Asp Gln
  1                5                10                15

```

```

Arg Gln Met Pro Arg Gln Arg Leu Pro Ser Ile Gln Glu Ile Phe Gly
      20      25      30
Glu Thr Phe Leu Ala Ile Pro Ser Asn Pro Ser Tyr Ala Leu Pro Ser
      35      40      45
His Thr Arg His Ala Ala Pro Pro Ala Leu Pro Ala Val Tyr Glu Ile
      50      55      60
Ala His Ser Ile Glu Gly Ala Pro Ser Asn Glu Gln Gly Leu Leu Pro
      65      70      75      80
Lys Ile Ser Thr Val Glu Arg Ser Leu Gly Ile Ile Ser Pro Val Asn
      85      90      95
Glu Leu Gln His Pro Glu Val Ile Arg Pro Glu Asn Pro Ser Phe Ser
      100      105      110
Pro Asn Gly Cys Ser Leu Asn Glu Ser Arg Arg Phe Ser Lys His Pro
      115      120      125
Asp Leu Ser Ile Pro Gln Pro Gly Leu Leu Ser Cys Asp Pro Met Asp
      130      135      140
Leu Ala Gln Pro Ser Phe Val Glu Pro Pro Asn Val Phe His Gly Phe
      145      150      155      160
Pro Ile Arg Lys Ile Pro Asn Ser Ile Pro Pro Gln Pro Lys Gln Leu
      165      170      175
Cys Leu Pro Glu Lys Arg Thr Pro Ser Ser Leu Asp Phe Ser Leu Phe
      180      185      190
Phe Lys Val Ile Glu Thr Val Ser Ala Gln Thr Leu Ala Phe Val Arg
      195      200      205
Tyr His Ser Ala Met Ser Gln Ser Asp Asn His Gln Arg Ser Leu Pro
      210      215      220
Gly Leu Ser Ile Thr Glu Ile Asn Gly Leu Leu Ser Gln Glu Gln Gln
      225      230      235      240
Lys Gln Asp Val Leu Ile Tyr Ile Arg Asp Glu Leu Val Arg Phe Asp
      245      250      255
Gln Tyr Gln Ala Leu Ala Gln Gln Asn Thr Arg Ala Ala Ala Cys Met
      260      265      270
Ala Gly Gly Ala Asp Arg Gly Leu Cys Ser Ser Val Thr Lys Gln Ser
      275      280      285
Lys Thr His Lys Val Ser Lys Gln Lys Arg Glu Trp His Gly Asp Ser
      290      295      300
Ala Leu Arg Cys His Ser Cys Asn Arg Ser Glu Thr Pro Glu Trp Arg
      305      310      315      320
Arg Gly Pro Asp Gly Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu His
      325      330      335
Tyr Ala Lys Leu Ser Arg Arg Thr Gly Lys Phe Val Ala Leu Asp Asp
      340      345      350
Ile Gly Ile Arg Gly Lys Thr
      355

```

<210> 69
 <211> 621
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 69
 atgtccggct acgaccagta caaccagggt ggctacggcc agcaagggtta tggccagcaa 60
 ggttacggcc agccagggtta cggccagcca ggttacggtg gtcaaccagg ttacggtggc 120

```

caggggtcacg accaacagca acagtacggt cagccccaac atgggtacgg ccagcaaggc 180
tacgggccagc aggggtggttc ttccgactac tacgccggcc agcaacacca gcagcagggt 240
tacgggccagc agcagggtgg ctcttccgac tactacgctg gccagcaaca ccagcagcat 300
ggctacggcc agcacgacca gaaccgtcag ggtggctacg agcagcagca gcatggtgcc 360
cccgatgagg ccaggatgg cgagcgtggt attgctggtg ccctcgcagg tggcgccgcc 420
ggtggcttcg ctggccacaa ggtcaaccac ggtttccttg gaacaatcgg cggagccatc 480
atcggtagca tcgctgaaga cgccgtcaag aagcacgca actccgacaa ccagtctcct 540
cctcagtacg gtggccccc tccttccaac agcggcagcg gtgggtccat gatggatcag 600
ctcggtggt tcttcaagaa g                                     621

```

<210> 70

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 70

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Met Ser Gly Tyr Asp Gln Tyr Asn Gln Gly Gly Tyr Gly Gln Gln Gly
 1           5           10           15
Tyr Gly Gln Gln Gly Tyr Gly Gln Pro Gly Tyr Gly Gln Pro Gly Tyr
 20           25           30
Gly Gly Gln Pro Gly Tyr Gly Gly Gln Gly His Asp Gln Gln Gln Gln
 35           40           45
Tyr Gly Gln Pro Gln His Gly Tyr Gly Gln Gln Gly Tyr Gly Gln Gln
 50           55           60
Gly Gly Ser Ser Asp Tyr Tyr Ala Gly Gln Gln His Gln Gln Gln Gly
 65           70           75           80
Tyr Gly Gln Gln Gln Gly Gly Ser Ser Asp Tyr Tyr Ala Gly Gln Gln
 85           90           95
His Gln Gln His Gly Tyr Gly Gln His Asp Gln Asn Arg Gln Gly Gly
 100          105          110
Tyr Glu Gln Gln Gln His Gly Ala Pro Asp Glu Ala Gln Asp Gly Glu
 115          120          125
Arg Gly Ile Ala Gly Ala Leu Ala Gly Gly Ala Ala Gly Gly Phe Ala
 130          135          140
Gly His Lys Val Asn His Gly Phe Leu Gly Thr Ile Gly Gly Ala Ile
 145          150          155          160
Ile Gly Ser Ile Ala Glu Asp Ala Val Lys Lys His Arg Asn Ser Asp
 165          170          175
Asn Gln Ser Pro Pro Gln Tyr Gly Gly Pro Pro Pro Ser Asn Ser Gly
 180          185          190
Ser Gly Gly Ser Met Met Asp Gln Leu Gly Gly Phe Phe Lys Lys
 195          200          205

```

<210> 71

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 71

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atgctgcacc tgggtgcaat tacctcccc gacccggagt tcaattcaga tgccccgagaa 60

```

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ttcttcactc gtcatatgag aattctcgag acatgctccg ccgcctggcc catgccggag 120
attcaggctc agatcgattc attaagactg gctttctccg ccgatatgca gcgtcctttc 180
gagttgaagc ccagtttccc atacggcagt ccctcggaac cctaccatcc cagtccacct 240
atggatgcgc actaccatcc gcacttgaat caaatccaat ccagagtgcg ttacaacccg 300
ctcccggcaa cccctccgat ttcggctggg gctgaagatt cgaagtccga cacatcttcc 360
cagatacaat ccctcgggat gggtgcccac cagccttcaa caactcatcc tctagatgcc 420
ccttcggtcg atgaaaatca ctgggacccg acccgaatca tcaactcaatg ggacatggcc 480
ttctccgtga acccttctac cgtcagcaca aactccccac caatgcctat aaacaattca 540
gtaccgagtg taaaaacgt tatgaacccc caatacccta tccaatacga gacacccaac 600
aaagtgccct ctgtcacatc taccactct ctctgcctt cgcagttcca gacacctcca 660
gttggtgttt cagcacgaga ctggcagcaa agtggttgcca gtgtgtatga tccacaaggg 720
ctgaaacggc gatggaatta tccagttgat gctagctccg acaataatat gtccaagcgc 780
caaagagga 789

```

<210> 72

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 72

```

Met Leu His Leu Val Ala Ile Thr Ser Pro Asp Pro Glu Phe Asn Ser
1          5          10          15
Asp Ala Arg Glu Phe Phe Thr Arg His Met Arg Ile Leu Glu Thr Cys
20          25          30
Ser Ala Ala Trp Pro Met Pro Glu Ile Gln Ala Gln Ile Asp Ser Leu
35          40          45
Arg Leu Ala Phe Ser Ala Asp Met Gln Arg Pro Phe Glu Leu Lys Pro
50          55          60
Ser Phe Pro Tyr Gly Ser Pro Ser Glu Pro Tyr His Pro Ser Pro Pro
65          70          75          80
Met Asp Ala His Tyr His Pro His Leu Asn Gln Ile Gln Ser Arg Val
85          90          95
Arg Tyr Asn Pro Leu Pro Ala Thr Pro Pro Ile Ser Ala Gly Ala Glu
100          105          110
Asp Ser Lys Ser Asp Thr Ser Ser Gln Ile Gln Ser Leu Gly Met Val
115          120          125
Ala His Gln Pro Ser Thr Thr His Pro Leu Asp Ala Pro Ser Val Asp
130          135          140
Glu Asn His Trp Asp Pro Thr Arg Ile Ile Thr Gln Trp Asp Met Ala
145          150          155          160
Phe Ser Val Asn Pro Ser Thr Val Ser Thr Asn Ser Pro Pro Met Pro
165          170          175
Ile Asn Asn Ser Val Pro Ser Val Gln Asn Val Met Asn Pro Gln Tyr
180          185          190
Pro Ile Gln Tyr Glu Thr Pro Asn Lys Val Pro Ser Val Thr Ser Thr
195          200          205
His Ser Leu Ser Pro Ser Gln Phe Gln Thr Pro Pro Val Val Phe Ser
210          215          220
Ala Arg Asp Trp Gln Gln Ser Val Ala Ser Val Tyr Asp Pro Gln Gly
225          230          235          240
Leu Lys Arg Arg Trp Asn Tyr Pro Val Asp Ala Ser Ser Asp Asn Asn
245          250          255
Met Ser Lys Arg Gln Arg Gly
260

```

<210> 73
 <211> 2745
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 73
 atggagccca acgaactttc cttcctgctc aagatggtcc agcgaacctc acaagagggc 60
 cagccccggg caaacggcat cagcgatgtc gcaaccccg atataggctc cgcacccgag 120
 cacatcatgt cgttcgatat caaggatgtc gtcgacattg ccgttccaaa cgttaccaca 180
 gctgaagttt cagccaagga accaaacggg gcttcccagg gtttcaggac agacagtgat 240
 atctccggaa acctagccat gcgagaacgc accttgcagc gctgggaacc ggctgagact 300
 gacattgata tgtcactcga aacgagcaat acttctgcgg gatgggatca gtttgaggca 360
 aacgagcgtc ttttcggcgc caagaccaac tacgatgaga acatctacac cactcgcctg 420
 gaccgttcgg atcccaacta caaacagaag caggcggagg cagctcggat cgcctcgtag 480
 attgagggac aagatgtgga caactccac atgcgcgagg agcgtggcct tgtagcacc 540
 gataccggtg accaagacga agaagacaag tacagtgttg ttcgcgcga agacaaagcc 600
 ttccctcccc ctacttcggg ccagccaaac aagtacatgc ccccgaggc cgcacaggca 660
 gcccacagt ctactgcgac tcccagtgca tccaccaaac agcctgttgc tccggttccc 720
 accgctccta tccccatccc ctctcaggcc gtggcgaagg aaactacacc agcagaccag 780
 caaactgagc tggtcgcctc tctgcaaccc acaacagata ccgagcagaa gagtgcctta 840
 ggcaaggggt tcacaccgcc agtatctact gcatcccccg caccagctgg aaagcggact 900
 gcacctgaaa atgcgaccgc aaacgtggag gtggaggtgc ttgatcactt ccggcagttc 960
 gcaaatagcg agaaaatcaa gatgcaggag cgccgtcgca accaggcctc gtatgaccgg 1020
 accatgaaac tcaatgagct gatgaagttt tccaagagct tcaaactctc cactccggtg 1080
 ccgaaagatc ttgttcctat cctagccaag gaccgactaa agcaagaagc aatcatgcaa 1140
 cgagcgtgc aacaagggga cgacaaggct acgccaagg tcaactacgc tcccacagag 1200
 caacaaccgc ctactcgtgg tgccggacat agtggagctg tgcccccatc cgcacccgct 1260
 gatcgtcaaa actacaaccg cactcgtcag ggtatcctc cagctgggtc gctcgtggt 1320
 gctggtggca gattccctca gcaagttcca ccgggacgtc ctggtgttgg catgctcagt 1380
 caccgactag cggacaatct gcagcaacga aagggcgcgg gtatgggacc tgttcccact 1440
 cctcttccca ttcaagatgc ccgtggaccc ccgactggc ctgccagcga tcagcagaga 1500
 atcaccagcc ctgtcaagtc gcaggccggg tcttctgcgg caaccaagtt taatgttaa 1560
 gctatggagt tcaagccaaa ccccgagcg agcactttca cccctggtac ctcggaact 1620
 gccgcaagcc caccgctttt ctctcgcaac cgctccgtgt caccgcgccac aaccocgact 1680
 gcgttctttg gctcaaggaa gccactgcct gtctccgaac gacctcgat cagtgaccaa 1740
 ttcaatccca tcaagcgcac gaagaaggag cacgcagaga ccgctgagag gttgattatg 1800
 ctgaatggag gtatccccc accctacaag actttgccaa cttgggacat cgcggacggc 1860
 agcgaagaga agacgtacga tgagatgttc aaacagcccg tcgccgttcc cacagtacca 1920
 cccaggggtc ggtcgtctc taacaacacc aatattcccc agcaacatca ggtgcccttc 1980
 cacttccagc aaggtaaccc agccatgccg ccatcttctg gcccttcgaa tggacctcat 2040
 ggccttcatt ctcaagggtc ccatggcccc tcccagtggt atgatcatca ccgcatgcag 2100
 ttatccgctg cgaactccca ggttttcccg tcccgcgga tgcaacatgg ataccatcc 2160
 cctatggctc cccatgcccc gctttccttc ccacaacgg tcccgagtt ttacggcggg 2220
 ccccaacctg gccatatcag acctttccag ggtgggtggtc ctcagtttgt gaatggcgct 2280
 cctatgatgg tgcagcaggc ctcgaaatgga coctacatgg gagtcccga aggcattgtc 2340
 ccctataacg cacagatgcc aatgtactcc ccgaacccag gccacgcta tccccacat 2400
 acacccagc ctcatagtgg gtaccaagc ccagccgtg gtgcgccc atgatgcac 2460
 cagaactcgc aatctggaca gcctcctcaa tcaatgatgt ttatgccgg ccaaccgggt 2520
 taccctcagc agtcgggaca catgcctccc aaccgtggca actaccaca gcagcctcac 2580
 ttttctcaa gtcccatca atcgcatcat tttccacct accagcatcg gacacccagc 2640
 aacggtttca accaaatgcc tcaaagcca cccagatgc ctgccgtac cccagcaaca 2700
 acccctggag cttctcacc ggccgaggca acggatgaag gaaaa 2745

<210> 74
 <211> 915
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 74

Met	Glu	Pro	Asn	Glu	Leu	Ser	Phe	Leu	Leu	Lys	Met	Val	Gln	Arg	Thr
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Ser	Gln	Glu	Gly	Gln	Pro	Arg	Ala	Asn	Gly	Ile	Ser	Asp	Val	Ala	Thr
			20					25					30		
Pro	Tyr	Ile	Gly	Ser	Ala	Pro	Glu	His	Ile	Met	Ser	Phe	Asp	Ile	Lys
		35					40					45			
Asp	Val	Val	Asp	Ile	Ala	Val	Pro	Asn	Val	Thr	Thr	Ala	Glu	Val	Ser
	50					55				60					
Ala	Lys	Glu	Pro	Asn	Gly	Ala	Ser	Gln	Gly	Phe	Arg	Thr	Asp	Ser	Asp
65					70				75					80	
Ile	Ser	Gly	Asn	Leu	Ala	Met	Arg	Glu	Arg	Thr	Leu	Gln	Arg	Trp	Glu
			85					90					95		
Pro	Ala	Glu	Thr	Asp	Ile	Asp	Met	Ser	Leu	Glu	Thr	Ser	Asn	Thr	Ser
			100					105					110		
Ala	Gly	Trp	Asp	Gln	Phe	Glu	Ala	Asn	Glu	Arg	Leu	Phe	Gly	Ala	Lys
		115					120					125			
Thr	Asn	Tyr	Asp	Glu	Asn	Ile	Tyr	Thr	Thr	Arg	Leu	Asp	Arg	Ser	Asp
	130					135					140				
Pro	Asn	Tyr	Lys	Gln	Lys	Gln	Ala	Glu	Ala	Ala	Arg	Ile	Ala	Arg	Glu
145					150					155					160
Ile	Glu	Gly	Gln	Asp	Val	Asp	Asn	Ser	His	Met	Arg	Glu	Glu	Arg	Gly
			165					170						175	
Leu	Val	Ala	Pro	Asp	Thr	Gly	Asp	Gln	Asp	Glu	Glu	Asp	Lys	Tyr	Ser
			180					185					190		
Gly	Val	Arg	Arg	Glu	Asp	Lys	Ala	Phe	Pro	Pro	Leu	Leu	Ser	Gly	Gln
		195					200					205			
Pro	Asn	Lys	Tyr	Met	Pro	Pro	Gly	Arg	Arg	Gln	Ala	Ala	Pro	Gln	Ser
	210					215					220				
Thr	Ala	Thr	Pro	Ser	Ala	Ser	Thr	Lys	Gln	Pro	Val	Ala	Pro	Val	Pro
225					230					235					240
Thr	Ala	Pro	Ile	Pro	Ile	Pro	Ser	Gln	Ala	Val	Ala	Lys	Glu	Thr	Thr
			245					250						255	
Pro	Ala	Asp	Gln	Gln	Thr	Glu	Leu	Val	Ala	Ser	Leu	Gln	Pro	Thr	Thr
			260					265					270		
Asp	Thr	Glu	Gln	Lys	Ser	Ala	Leu	Gly	Lys	Gly	Val	Thr	Pro	Pro	Val
		275					280					285			
Ser	Thr	Ala	Ser	Pro	Ala	Pro	Ala	Gly	Lys	Arg	Thr	Ala	Pro	Glu	Asn
	290					295					300				
Ala	Thr	Ala	Asn	Val	Glu	Val	Glu	Val	Leu	Asp	His	Phe	Arg	Gln	Phe
305					310					315					320
Ala	Asn	Ser	Glu	Lys	Ile	Lys	Met	Gln	Glu	Arg	Arg	Arg	Asn	Gln	Ala
			325					330						335	
Ser	Tyr	Asp	Arg	Thr	Met	Lys	Leu	Asn	Glu	Leu	Met	Lys	Phe	Ser	Lys
			340					345					350		
Ser	Phe	Lys	Leu	Ser	Thr	Pro	Val	Pro	Lys	Asp	Leu	Val	Pro	Ile	Leu
		355					360					365			
Ala	Lys	Asp	Arg	Leu	Lys	Gln	Glu	Ala	Ile	Met	Gln	Arg	Ala	Leu	Gln

370		375		380
Gln Gly Asp Asp Lys Ala Thr Pro Lys Val Thr Thr Pro Pro Thr Glu				
385		390		400
Gln Gln Pro Pro Thr Arg Gly Ala Gly Pro Ser Gly Ala Val Pro Pro				
	405		410	415
Ser Ala Pro Ala Asp Arg Gln Asn Tyr Asn Arg Thr Arg Gln Gly Tyr				
	420		425	430
Pro Pro Ala Gly Pro Leu Ala Gly Ala Gly Gly Arg Phe Pro Gln Gln				
	435		440	445
Val Pro Pro Gly Arg Pro Gly Val Gly Met Leu Ser His Arg Leu Ala				
	450		455	460
Asp Asn Leu Gln Gln Arg Lys Gly Ala Gly Met Gly Pro Val Pro Thr				
465		470		480
Pro Leu Pro Ile Gln Asp Ala Arg Gly Pro Pro Thr Gly Pro Ala Ser				
	485		490	495
Asp Gln Gln Arg Ile Thr Ser Pro Val Lys Ser Gln Ala Gly Ser Ser				
	500		505	510
Ala Ala Thr Lys Phe Asn Val Lys Ala Met Glu Phe Lys Pro Asn Pro				
	515		520	525
Ala Ala Ser Thr Phe Thr Pro Gly Thr Ser Gly Thr Ala Ala Ser Pro				
	530		535	540
Arg Pro Phe Ser Arg Asn Arg Ser Val Ser Arg Ala Thr Thr Pro Thr				
545		550		560
Ala Phe Phe Gly Ser Arg Lys Pro Leu Pro Val Ser Glu Arg Pro Ser				
	565		570	575
Ile Ser Asp Gln Phe Asn Pro Ile Lys Arg Met Lys Lys Glu His Ala				
	580		585	590
Glu Thr Ala Glu Arg Leu Ile Met Leu Asn Gly Gly Ile Pro Pro Pro				
	595		600	605
Tyr Lys Thr Leu Pro Thr Trp Asp Ile Ala Asp Gly Ser Glu Glu Lys				
	610		615	620
Thr Tyr Asp Glu Met Phe Lys Gln Pro Val Ala Val Pro Thr Val Pro				
625		630		640
Pro Gln Gly Arg Ser Val Ser Asn Asn Thr Asn Ile Pro Gln Gln His				
	645		650	655
Gln Val Pro Phe His Phe Gln Gln Gly Asn Pro Ala Met Pro Pro Ser				
	660		665	670
Ser Gly Pro Ser Asn Gly Pro His Gly Leu His Ser Gln Gly Pro His				
	675		680	685
Gly Pro Ser His Val Asp Asp His His Arg Met Gln Leu Ser Ala Ser				
	690		695	700
Asn Ser Gln Val Phe Pro Ser Pro Arg Met Gln His Gly Tyr Pro Ser				
705		710		720
Pro Met Ala Pro His Ala Gln Leu Ser Phe Pro Gln Pro Val Pro Gln				
	725		730	735
Phe Tyr Gly Gly Pro Gln Pro Gly His Ile Arg Pro Phe Gln Gly Gly				
	740		745	750
Gly Pro Gln Phe Val Asn Gly Ala Pro Met Met Val Gln Gln Ala Ser				
	755		760	765
Asn Gly Pro Tyr Met Gly Val Pro Gln Gly Met Ser Pro Tyr Asn Ala				
	770		775	780
Gln Met Pro Met Tyr Ser Pro Asn Pro Gly His Ala Tyr Pro Gln His				
785		790		800
Thr Pro Gln Pro His Ser Gly Tyr Pro Ser Pro Ser Arg Gly Ala Pro				
	805		810	815
Met Met Met His Gln Asn Ser Gln Ser Gly Gln Pro Pro Gln Ser Met				
	820		825	830

Met Phe Met Pro Gly Gln Pro Gly Tyr Pro Gln Gln Ser Gly His Met
 835 840 845
 Pro Pro Asn Arg Gly Asn Tyr Pro Gln Gln Pro His Phe Ser Ser Ser
 850 855 860
 Pro His Gln Ser His His Phe Pro Pro Asn Gln His Arg Thr Pro Ser
 865 870 875 880
 Asn Gly Phe Asn Gln Met Pro Gln Met Pro Pro Gln Met Pro Ala Ala
 885 890 895
 Thr Pro Ala Thr Thr Pro Gly Ala Ser His Pro Ala Glu Ala Thr Asp
 900 905 910
 Glu Gly Lys
 915

<210> 75
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 75
 atgggttttg ctcagaaaaat cgccgcagct cagaatagcc agaacatggc taacagtggg 60
 tcatatggag gtgcacctcc gtcaggatac actgggggtc ctctgcccgc tctgcagcct 120
 ggtggatcga gccaacagcc ccaataccag gcttattcag gatccccagc ccccaggga 180
 tcggcaccac cctaccctac ccagggttcc ccgtaccccg gtggccaggg ccgtcctggg 240
 ccctcaccag gaccaccaag cggaccgccc ccaggccaat atgggcgcacc cgggtggcgcc 300
 cctccctccg catctcccc ggccactcag caacagggtcg cagcctaccg atcgcttttg 360
 atttccgcga ttcaggagaa gaacctccaa agcttctacc ctcccagagc actggaccga 420
 ctcgttcagt cgcttgccgc tgaagcacca ggcaagctca ataggctgat tcatgaatgg 480
 gccgtgccta tggaggttgc gaccgatgtc atgaagcttt cgctgtttga cgtggttctc 540
 tatgttgatg acagtggatc tatcgaattc gaagagaagg gactccgaaa ggaccagctc 600
 aaacaaattc tcggcatcgt agctactgcc gcatctacct ttgaccagga tggatattct 660
 gtccgattca tgaactccag cgagaaggcc gatggcatcc gcaatgcaga ggatgtcgag 720
 cgccatagtgt cccgagtcgg tttttcaggc ctgacccctc tgggcaccag tctgaggagc 780
 aaagtcatcg accccatggt tgttcaaccc gccaggcca accgtctcga caagcccgtt 840
 ctggtgatca ccatcacgga cggacagcct gctggcgagc ctcatggtac cgtgggtgat 900
 gtcattcgct acgcagtggg ggagacgtca cggaccggtt atggccccgg caccgtagcc 960
 ttccagttct cgcagggtgg aactgatcag cgggctcgcg acttcttggg ctctctggat 1020
 gaggaccctc atatcggcc tctgatcgac tgtacttcca actttgaggt tgagcaggat 1080
 gagatgtcgc gtgctaacc acccgtgcat ctactcgcg agctttgggt ccccaactg 1140
 atgctcgcg ctatcgattc ttcttacgac accaaggatg agcgagagaa tcaacgtcgt 1200
 ggtgcacccc caccaacagg ccagtacgga ggagggtacg gccaacctcc gccaccccag 1260
 ggccaagctc agcctcogta tggtcgccc cctggtgccc caccggcttc gtacggttct 1320
 cagccaggct acccacgca gggccaatac caacagcctc cccagcagcc tccctaccag 1380
 ggatcgcggg gtgggtatgg ccaacagcag ccacatgggt atggatcccc tggacctggc 1440
 taccgatatg gtggacagcc gccacgctat 1470

<210> 76
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 76

Met	Gly	Phe	Ala	Gln	Lys	Ile	Ala	Ala	Ala	Gln	Asn	Ser	Gln	Asn	Met
1				5					10					15	
Ala	Asn	Ser	Gly	Ser	Tyr	Gly	Gly	Ala	Pro	Pro	Ser	Gly	Tyr	Thr	Gly
			20					25					30		
Gly	Pro	Pro	Ala	Ala	Leu	Gln	Pro	Gly	Gly	Ser	Ser	Gln	Gln	Pro	Gln
		35					40					45			
Tyr	Gln	Ala	Tyr	Ser	Gly	Ser	Pro	Ala	Pro	Gln	Gly	Ser	Ala	Pro	Pro
	50					55					60				
Tyr	Pro	Thr	Gln	Gly	Ser	Pro	Tyr	Pro	Gly	Gly	Gln	Gly	Arg	Pro	Gly
65					70				75					80	
Pro	Ser	Pro	Gly	Pro	Pro	Ser	Gly	Pro	Pro	Pro	Gly	Gln	Tyr	Gly	Ala
				85					90					95	
Pro	Gly	Gly	Ala	Pro	Pro	Ser	Ala	Ser	Pro	Pro	Ala	Thr	Gln	Gln	Gln
			100					105					110		
Val	Ala	Ala	Tyr	Arg	Ser	Leu	Leu	Ile	Ser	Ala	Ile	Gln	Glu	Lys	Asn
		115					120					125			
Leu	Gln	Ser	Phe	Tyr	Pro	Pro	Glu	Arg	Leu	Asp	Arg	Leu	Val	Gln	Ser
	130					135					140				
Leu	Ala	Ala	Glu	Ala	Pro	Gly	Lys	Leu	Asn	Arg	Leu	Ile	His	Glu	Trp
145					150					155				160	
Ala	Val	Pro	Met	Glu	Val	Ala	Thr	Asp	Val	Met	Lys	Leu	Ser	Leu	Phe
				165					170					175	
Asp	Val	Val	Leu	Tyr	Val	Asp	Asp	Ser	Gly	Ser	Ile	Glu	Phe	Glu	Glu
			180					185					190		
Lys	Gly	Leu	Arg	Lys	Asp	Gln	Leu	Lys	Gln	Ile	Leu	Gly	Ile	Val	Ala
		195					200					205			
Thr	Ala	Ala	Ser	Thr	Phe	Asp	Gln	Asp	Gly	Ile	Ser	Val	Arg	Phe	Met
	210					215					220				
Asn	Ser	Ser	Glu	Lys	Gly	Asp	Gly	Ile	Arg	Asn	Ala	Glu	Asp	Val	Glu
225					230					235				240	
Arg	Leu	Val	Ser	Arg	Val	Arg	Phe	Ser	Gly	Leu	Thr	Pro	Leu	Gly	Thr
				245					250					255	
Ser	Leu	Arg	Ser	Lys	Val	Ile	Asp	Pro	Met	Val	Val	Gln	Pro	Ala	Gln
			260					265					270		
Ala	Asn	Arg	Leu	Asp	Lys	Pro	Val	Leu	Val	Ile	Thr	Ile	Thr	Asp	Gly
		275					280					285			
Gln	Pro	Ala	Gly	Glu	Pro	His	Gly	Thr	Val	Gly	Asp	Val	Ile	Arg	Tyr
	290					295					300				
Ala	Val	Glu	Glu	Thr	Ser	Arg	Thr	Arg	Tyr	Gly	Pro	Gly	Thr	Val	Ala
305					310					315				320	
Phe	Gln	Phe	Ser	Gln	Val	Gly	Thr	Asp	Gln	Arg	Ala	Arg	Asp	Phe	Leu
				325					330					335	
Gly	Ser	Leu	Asp	Glu	Asp	Pro	His	Ile	Gly	His	Leu	Ile	Asp	Cys	Thr
			340					345					350		
Ser	Asn	Phe	Glu	Val	Glu	Gln	Asp	Glu	Met	Ser	Arg	Ala	Asn	Pro	Pro
		355					360					365			
Val	His	Leu	Thr	Arg	Glu	Leu	Trp	Cys	Pro	Lys	Leu	Met	Leu	Gly	Ala
	370					375					380				
Ile	Asp	Ser	Ser	Tyr	Asp	Thr	Lys	Asp	Glu	Arg	Glu	Asn	Gln	Arg	Arg
385					390					395				400	
Gly	Ala	Pro	Pro	Pro	Thr	Gly	Gln	Tyr	Gly	Gly	Gly	Tyr	Gly	Gln	Pro
				405					410					415	
Pro	Pro	Pro	Gln	Gly	Gln	Ala	Gln	Pro	Pro	Tyr	Gly	Pro	Pro	Pro	Gly
			420					425					430		
Ala	Pro	Pro	Ala	Ser	Tyr	Gly	Ser	Gln	Pro	Gly	Tyr	Pro	Pro	Gln	Gly
		435					440					445			

Gln Tyr Gln Gln Pro Pro Gln Gln Pro Pro Tyr Gln Gly Ser Arg Gly
 450 455 460
 Gly Tyr Gly Gln Gln Gln Pro His Gly Tyr Gly Ser Pro Gly Pro Gly
 465 470 475 480
 Tyr Gln Tyr Gly Gly Gln Pro Pro Arg Tyr
 485 490

<210> 77
 <211> 1215
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 77
 atgcaaagcc cccagcagcc acccgacttt ctactgtacc cgactcagtc cacgcgtggg 60
 agcaaaatga tcgccttgga ttcggtccgc cagcagcaga cccattctt ccagaatttc 120
 accatggatc ctgcattcac ggaccctttc gcattccagg tggacacctt cgctagcttc 180
 ggacagcccg ccagttcctc tcgaggcccc cagacttcat attatgatac ccctccgctc 240
 tacacggatt cttactccga ctccaataag accgcccctg ggtttccttc catgccgggt 300
 acgccccga cgcttccctc caccagccg ctggactccc acgttcggg cctgaccgcc 360
 ccgtcgggtc cgtctgtcgc cagcgctcc tcctcgcca ttgggtcgcc gtactccgpc 420
 acggcccatg ccaaccagga gaactgggtc gatacgaacc acggcctggg ccttcccgcc 480
 gcggtgatgg gggatctgtt tccgaacgac tacacgggga cgaccctgga ccccgattac 540
 tttgccaata aaggcgcgga cagctttgtt gacccttctt tgatcccgct tcagcagcag 600
 tcgaatctgt cgaccccggc catctcctac ccggaacaga ctgattatag cctgggtccc 660
 ggcggtattc tccctcagtc ccctgaccct tccaattcc aatttgcgga cccctatggg 720
 ccattcacac agcagccatg ccccatgccc gcctcatccc catctctgat gccctcccat 780
 gtcccgcgcc gtgctctctc cctctacgac cgtcggtcct cgggtctctc cgtgcagtc 840
 cgtcgtcgc agctgagccc ggcgccagc aacgccgaga tcgaggagga cgccaaggaa 900
 aagggccgat gccctcatcc ggattgcggg cgagtcttcc gggacctgaa agcgcacatg 960
 ctgacgcatac agtcggagcg tccggagaaa tgccccattg tcacttgcca gtaccacacc 1020
 aagggtttg cccgcaagta cgacaagaac cgccacacc tgaccacta caagggaacg 1080
 atggtttgcg gcttctgccc gggatccggg tcgcccggcg agaagagctt caaccgggcg 1140
 gatgtgttca aacgtcatct gacctctgtg cacggtgtgg aacagacccc tcccaactgc 1200
 cggaagagaa gcccc 1215

<210> 78
 <211> 405
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 78
 Met Gln Ser Pro Gln Gln Pro Pro Asp Phe Leu Leu Tyr Pro Thr Gln
 1 5 10 15
 Ser Thr Arg Gly Ser Lys Met Ile Ala Leu Asp Ser Ser Arg Gln Gln
 20 25 30
 Gln Thr Pro Phe Phe Gln Asn Phe Thr Met Asp Pro Ala Phe Thr Asp
 35 40 45
 Pro Phe Ala Phe Gln Val Asp Thr Phe Ala Ser Phe Gly Gln Pro Ala
 50 55 60
 Ser Ser Ser Arg Gly Pro Gln Thr Ser Tyr Tyr Asp Thr Pro Pro Leu

65					70					75					80
Tyr	Thr	Asp	Ser	Tyr	Ser	Asp	Ser	Asn	Lys	Thr	Ala	Pro	Gly	Phe	Pro
				85					90					95	
Ser	Met	Pro	Gly	Thr	Pro	Pro	Thr	Leu	Pro	Ser	Thr	Gln	Pro	Leu	Asp
			100					105					110		
Ser	His	Val	Pro	Gly	Leu	Thr	Ala	Pro	Ser	Gly	Pro	Ser	Val	Ala	Ser
			115				120					125			
Ala	Ser	Ser	Ser	Ala	Ile	Gly	Ser	Pro	Tyr	Ser	Gly	Thr	Ala	His	Ala
			130			135					140				
Asn	Gln	Glu	Asn	Trp	Val	Asp	Thr	Asn	His	Gly	Leu	Gly	Leu	Pro	Ala
145					150					155					160
Ala	Val	Met	Gly	Asp	Leu	Phe	Pro	Asn	Asp	Tyr	Thr	Gly	Thr	Thr	Leu
				165					170					175	
Asp	Pro	Asp	Tyr	Phe	Ala	Asn	Lys	Gly	Ala	Asp	Ser	Phe	Val	Asp	Pro
			180					185					190		
Ser	Leu	Ile	Pro	Leu	Gln	Gln	Gln	Ser	Asn	Leu	Ser	Thr	Pro	Ala	Ile
		195					200					205			
Ser	Tyr	Pro	Glu	Gln	Thr	Asp	Tyr	Ser	Leu	Val	Pro	Gly	Gly	Phe	Phe
210						215					220				
Pro	Gln	Ser	Pro	Asp	Pro	Ser	Gln	Phe	Gln	Phe	Ala	Asp	Pro	Tyr	Gly
225					230					235					240
Pro	Phe	Thr	Gln	Gln	Pro	Cys	Pro	Met	Pro	Ala	Ser	Ser	Pro	Ser	Leu
				245					250					255	
Met	Pro	Ser	His	Val	Pro	Pro	Arg	Arg	Leu	Ser	Leu	Tyr	Asp	Arg	Arg
			260					265					270		
Ser	Ser	Val	Ser	Ser	Val	Gln	Ser	Arg	Arg	Ser	Gln	Leu	Ser	Pro	Ala
		275					280					285			
Ala	Ser	Asn	Ala	Glu	Ile	Glu	Glu	Asp	Ala	Lys	Glu	Lys	Gly	Arg	Cys
290						295					300				
Pro	His	Pro	Asp	Cys	Gly	Arg	Val	Phe	Arg	Asp	Leu	Lys	Ala	His	Met
305				310						315					320
Leu	Thr	His	Gln	Ser	Glu	Arg	Pro	Glu	Lys	Cys	Pro	Ile	Val	Thr	Cys
				325					330					335	
Glu	Tyr	His	Thr	Lys	Gly	Phe	Ala	Arg	Lys	Tyr	Asp	Lys	Asn	Arg	His
			340					345					350		
Thr	Leu	Thr	His	Tyr	Lys	Gly	Thr	Met	Val	Cys	Gly	Phe	Cys	Pro	Gly
		355					360					365			
Ser	Gly	Ser	Pro	Ala	Glu	Lys	Ser	Phe	Asn	Arg	Ala	Asp	Val	Phe	Lys
370						375					380				
Arg	His	Leu	Thr	Ser	Val	His	Gly	Val	Glu	Gln	Thr	Pro	Pro	Asn	Cys
385					390					395					400
Arg	Lys	Arg	Ser	Pro											
				405											

<210> 79

<211> 1389

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 79

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atggagacgt actacggcca tgtccgcact cctgcggacg ccatacatcct cttcgaggcc 60
tgtcgatttg gtcttctccc tcgctccag cgtcgactgt ccgagaaaga acggcagttg 120
atccgctctg ggtccgtctt tgtctgggat gagcgagaag ccggcatgcg ccgctggacg 180

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gacggcaagt cctggagcgc cagtcgcgtg tctggcagct ttctcacgta tcgcgagatg 240
gaaggcaagc gaggaggcac cggagtatcg cagagcacca ttccgcgagc cgggaaaact 300
cccgagagca cccgcggcag tgacgacgac cgcggcgatg gcgcagacga aggccccgat 360
gggtaccgat ataagcccga cggcttgatg aagcagtcct tcagtatcac cacctccgcc 420
ggccaacacc tccatctcat cagctactac tcgcgctccc atccgtccgc cgccaacctg 480
caacagccca ccaacgatcc caccctgcgc catgttcgac ccagaaaagg cctctatccc 540
gaatccacgg tcaacgacca gcagaacctg cccgtcgtga ctgcgggccc catgggcggt 600
gcttactccg tccaccaccc catgectccc tacgctcgct ccggcgccac gcatccgcaa 660
tcatacactc cgccctatgc ctggcccccg acgccgctgg ccaccccgcc cgtcaccgtc 720
cattactcgc catacctccc gccgggtgctg ggcgccaacg gccaaactcta cgctcatcat 780
catcaacccc cgcagccggg gctgccgccc ccgccccgcg cgcagccagg cctgtccgcc 840
gcctacgaac gcccgtgca cctatcgag agcgtatcg cgcgcggcgc catccatgcc 900
tcggcgctcc accatcctgc gctccctgtg atcgccggcc gctccccgcg tctcgtcgcc 960
gacgcccacg acgtccacca gcgcagcccg cccgcctacg cggccaccga cccccggcgc 1020
gcctctccgc gcacccaacc gccccccatc cccgcaacaa acggctacgg cccggccgca 1080
cgcagcccag ccacgctgac ccagccggcg ccgcccaccg cgcgcggccc gcagcagcag 1140
cagcctccat cgacatcggc tcaaattccc cgcccaagc tcgccgaacc ctccaccacg 1200
gggaccacgg taccacagcat cggggccctg atgaacggcg ccgcagccgg cggcggcctg 1260
ccctccatca cggccacggc agcgtcgacc ggccgcggcg acgggccccg cgatatcccc 1320
agcgagaaga tcgggttcgg cggcgaggat atgcgcgcgc tccgacaatt ggaccgcgtg 1380
ttcacggcg                                     1389

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<210> 80

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 80

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Met Glu Thr Tyr Tyr Gly His Val Arg Thr Pro Ala Asp Ala Ile Ile
 1             5             10             15
Leu Phe Glu Ala Cys Arg Ile Gly Leu Leu Pro Arg Val Gln Arg Arg
      20             25             30
Leu Ser Glu Lys Glu Arg Gln Leu Ile Arg Ser Gly Ser Val Phe Val
      35             40             45
Trp Asp Glu Arg Glu Ala Gly Met Arg Arg Trp Thr Asp Gly Lys Ser
      50             55             60
Trp Ser Ala Ser Arg Val Ser Gly Ser Phe Leu Thr Tyr Arg Glu Met
      65             70             75             80
Glu Gly Lys Arg Gly Gly Thr Gly Val Ser Gln Ser Thr Ile Pro Arg
      85             90             95
Ala Gly Lys Thr Pro Glu Ser Thr Arg Gly Ser Asp Asp Asp Arg Gly
      100            105            110
Asp Gly Ala Asp Glu Gly Pro Asp Gly Tyr Arg Tyr Lys Pro Asp Gly
      115            120            125
Leu Met Lys Gln Ser Phe Ser Ile Thr Thr Ser Ala Gly Gln His Leu
      130            135            140
His Leu Ile Ser Tyr Tyr Ser Arg Ser His Pro Ser Ala Ala Asn Leu
      145            150            155            160
Gln Gln Pro Thr Asn Asp Pro Thr Leu Arg His Val Arg Pro Gln Lys
      165            170            175
Gly Leu Tyr Pro Glu Ser Thr Val Asn Asp Gln Gln Asn Leu Pro Val
      180            185            190
Val Thr Arg Gly Pro Met Gly Gly Ala Tyr Ser Val His His Pro Met
      195            200            205

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Pro Pro Tyr Ala Arg Ser Gly Ala Thr His Pro Gln Ser Tyr Thr Pro
 210 215 220
 Pro Tyr Ala Trp Pro Pro Thr Pro Leu Ala Thr Pro Pro Val Thr Val
 225 230 235 240
 His Tyr Ser Pro Tyr Leu Pro Pro Val Ser Gly Ala Asn Gly Gln Leu
 245 250 255
 Tyr Ala His His His Gln Pro Pro His Ala Gly Leu Pro Pro Pro Pro
 260 265 270
 Pro Pro Gln Pro Gly Leu Ser Ala Ala Tyr Glu Arg Pro Val His Pro
 275 280 285
 Ile Glu Ser Ala Ile Ala Pro Ala Ile His Ala Ser Gly Val His
 290 295 300
 His Pro Ala Leu Pro Val Ile Ala Gly Arg Ser Pro Arg Leu Val Ala
 305 310 315 320
 Asp Ala His Asp Val His Gln Arg Ser Pro Pro Ala Tyr Ala Ala Thr
 325 330 335
 Asp Pro Arg Arg Ala Ser Pro Arg Thr Gln Pro Pro Pro Ile Pro Ala
 340 345 350
 Thr Asn Gly Tyr Gly Pro Ala Ala Arg Ser Pro Ala Thr Leu Thr Gln
 355 360 365
 Pro Pro Pro Pro Pro Pro Pro Gln Gln Gln Gln Pro Pro Ser
 370 375 380
 Thr Ser Ala Gln Ile Pro Pro Pro Lys Leu Ala Glu Pro Ser Thr Thr
 385 390 395 400
 Gly Thr Thr Val Pro Ser Ile Gly Ala Leu Met Asn Gly Ala Ala Ala
 405 410 415
 Gly Gly Gly Leu Pro Ser Ile Thr Ala Thr Ala Ala Ser Thr Gly Arg
 420 425 430
 Ala Asp Gly Pro Arg Asp Ile Pro Ser Glu Lys Ile Gly Phe Gly Gly
 435 440 445
 Glu Asp Met Arg Ala Leu Arg Gln Leu Asp Arg Val Phe Thr Ala
 450 455 460

<210> 81
 <211> 2055
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 81
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 gctgctttgt ccactttctc tccatcttta cttaattctt ccaactgtcg atctgtcgac 120
 tcgaaccctt caaaccgcgt gttcagaaag agcgaaacct ttcatgcagc gagaaaccgt 180
 cccacccac gcgactctcg tctcagcttg cctcttgac cccgccgctc tcctacatct 240
 cccgctgccc tcgaagccat cgcggccggc agagagcgca tgagcaagat cctcgatacc 300
 ctcgacctcg ataccttcac tccctcggaa tccgttgatg aggaactccc cgtgccccgc 360
 agtgtcttgc aacttcattt cgactctttg catatctcgg accctcccca gagtccgtcc 420
 gtccgttcag ctcccaagaa gccgctccaa agagtcaacc atcacacttc cgacagcggg 480
 ctcgggacct ctgtttgtag cgaagaagcg ctgtcttgta ccgaatccgc cgatctggac 540
 tcgaacgccc ccatgtccgc ctcacatctt cggaaattgt cgcctgacgg ggtcgacaag 600
 atagagcacc gtgtcttcta ccctcttctt atgaacacgc agttcgataa gttccacagc 660
 actgttcgat atgccgctca aggggtcaag gacaatcgat tccgctgtct ccgtgacgtg 720
 gaaaatttat tccgcaatcc attccctatt gaccatgtta atgagaagga ggaattttct 780
 cttttcctga atcaggtggg cctgtgcctc gacgacactt ggcaccgcct cgatgaatcg 840


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gaccgcacta tgcctgggtga tgtcccgtac tcgaatgagt acatcctcga cctttacgat 900
caaatcgtcc gcttcaaggc gctctgtgag cgagcgaaac agactctctc gcagacggat 960
agcaacagtg ccaccccaa gttgcccaag ctctgtgtca aaggcggctt ggccaaaaca 1020
ggacgccagg cggaactggt cgctcagtcg gatgaccaga tgatgtcgct ccgcacgggt 1080
aaaccctacc aggagagcca ggtgccgagc atgaagcgtg gcctcagcct atgtctgacg 1140
gatggagagg gcgcccaccg atgcatggcc cgccgccgga agaacgaggc tcccatgaac 1200
atcaacactc cgtgcgactt ttgcgggcaa attttcgcga gacctgtga cctcactaaa 1260
cacatgaaga cccacacacg cccgttcaag tgttcggtgc ctgagtgcaa gtactacacc 1320
tatggattcc cgactgaaaa ggagaaagac cgtcatttca acgacaagca caaccccgac 1380
ccggaaccgt acgaatgcga tctgggagga tgcaattatc gctctaagcg gttgagtaat 1440
ttgaagcagc ataaggagaa gaagcacggc tggcaatacy tccggaccaa gagcaacggc 1500
aagcgcaagg agaagggcaa gggcaagaaa gccagtcctc agtctactcc ggatactccc 1560
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gatcctccgt tgcccacccc gggtgcggac ttccaactgt tcaacgcgaa cagccccatg 1740
ggagggaaac gaagcgtgaa catgggttat gcggatttgg gctttccgga aatgactcgg 1800
tcaatggacg gcgacgtggt tcatatgaac aactttgaag acatgttcgc caacgtcaac 1860
aacccttacc tggatggact cagcgggggt tatcaagtcc ccagcggcta tgaagccggc 1920
aacattgact ttccgcatct gggttatggc acggccgtgc ctccgtctgc ggtcttccac 1980
gaagaccaat tctgcccgga gacgatcaac tgggaagaat tcgccatgct taacggaatg 2040
gatacgatgt ccaag                                     2055

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<210> 82

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 82

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Met Ser Ser Pro Lys Asp Ser Gln Tyr Asp Thr Thr Leu Arg Arg His
1          5          10          15
Pro Arg Arg Arg Ala Ala Leu Ser Thr Ser Pro Pro Ser Leu Leu Asn
20          25          30
Ser Ser Asn Cys Arg Ser Val Asp Ser Asn Pro Ser Asn Pro Leu Phe
35          40          45
Arg Lys Ser Glu Thr Phe His Ala Ala Arg Asn Arg Pro Thr Pro Arg
50          55          60
Asp Pro Arg Leu Ser Leu Pro Leu Ala Pro Arg Arg Ser Pro Thr Ser
65          70          75          80
Pro Ala Ala Leu Glu Ala Ile Ala Ala Gly Arg Glu Arg Met Ser Lys
85          90          95
Ile Leu Asp Thr Leu Asp Leu Asp Thr Phe Thr Pro Ser Glu Ser Val
100         105         110
Asp Glu Glu Leu Pro Val Pro Arg Ser Val Leu Gln Leu His Phe Asp
115         120         125
Ser Leu His Ile Ser Asp Pro Pro Gln Ser Pro Ser Val Arg Ser Ala
130         135         140
Pro Lys Lys Pro Leu Gln Arg Val Asn His His Thr Ser Asp Ser Gly
145         150         155         160
Leu Gly Thr Ser Val Cys Ser Glu Glu Ala Leu Ser Cys Thr Glu Ser
165         170         175
Ala Asp Leu Asp Ser Asn Ala Pro Met Ser Ala Ser His Leu Arg Lys
180         185         190
Leu Ser Pro Asp Gly Val Asp Lys Ile Glu His Arg Val Phe Tyr Pro
195         200         205

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Leu Leu Met Asn Thr Gln Phe Asp Lys Phe His Ser Thr Val Arg Tyr
 210 215 220
 Ala Ala Gln Gly Val Lys Asp Asn Arg Phe Arg Cys Leu Arg Asp Val
 225 230 235 240
 Glu Asn Leu Phe Arg Asn Pro Phe Pro Ile Asp His Val Asn Glu Lys
 245 250 255
 Glu Glu Phe Ser Leu Phe Leu Asn Gln Val Val Leu Cys Leu Asp Asp
 260 265 270
 Thr Trp His Arg Leu Asp Glu Ser Asp Arg Thr Met Pro Gly Asp Val
 275 280 285
 Pro Tyr Ser Asn Glu Tyr Ile Leu Asp Leu Tyr Asp Gln Ile Val Arg
 290 295 300
 Phe Lys Ala Leu Cys Glu Arg Ala Lys Gln Thr Leu Ser Gln Thr Asp
 305 310 315 320
 Ser Asn Ser Ala Thr Pro Lys Leu Pro Lys Leu Val Phe Lys Gly Gly
 325 330 335
 Leu Ala Lys Thr Gly Arg Gln Ala Glu Leu Val Ala Gln Ser Asp Asp
 340 345 350
 Gln Met Met Ser Leu Arg Thr Gly Lys Pro Tyr Gln Glu Ser Gln Val
 355 360 365
 Pro Ser Met Lys Arg Gly Leu Ser Leu Cys Ser Thr Asp Gly Glu Gly
 370 375 380
 Ala His Arg Cys Met Ala Arg Arg Arg Lys Asn Glu Ala Pro Met Asn
 385 390 395 400
 Ile Asn Thr Pro Cys Asp Phe Cys Gly Gln Ile Phe Ala Arg Pro Cys
 405 410 415
 Asp Leu Thr Lys His Met Lys Thr His Thr Arg Pro Phe Lys Cys Ser
 420 425 430
 Val Pro Glu Cys Lys Tyr Tyr Thr Tyr Gly Phe Pro Thr Glu Lys Glu
 435 440 445
 Lys Asp Arg His Phe Asn Asp Lys His Asn Pro Asp Pro Glu Pro Tyr
 450 455 460
 Glu Cys Asp Leu Gly Gly Cys Asn Tyr Arg Ser Lys Arg Leu Ser Asn
 465 470 475 480
 Leu Lys Gln His Lys Glu Lys Lys His Gly Trp Gln Tyr Val Arg Thr
 485 490 495
 Lys Ser Asn Gly Lys Arg Lys Glu Lys Gly Lys Gly Lys Lys Ala Ser
 500 505 510
 Pro Gln Ser Thr Pro Asp Thr Pro Gly Leu Thr Thr Pro Gly Thr Ser
 515 520 525
 Thr Ala Gln Ser Phe Ser Thr Pro Asn Thr Gly Pro Ser Pro Ser Pro
 530 535 540
 Pro Gln Ala Val Ser Arg Pro Leu Pro Thr Thr Asp Phe Asn Phe Ala
 545 550 555 560
 Asp Pro Pro Leu Pro Thr Pro Val Ala Asp Phe Gln Leu Phe Asn Ala
 565 570 575
 Asn Ser Pro Met Gly Gly Asn Gly Ser Val Asn Met Gly Tyr Ala Asp
 580 585 590
 Leu Gly Phe Pro Glu Met Thr Arg Ser Met Asp Gly Asp Val Val His
 595 600 605
 Met Asn Asn Phe Glu Asp Met Phe Ala Asn Val Asn Asn Pro Tyr Leu
 610 615 620
 Asp Gly Leu Ser Gly Gly Tyr Gln Val Pro Ser Gly Tyr Glu Ala Gly
 625 630 635 640
 Asn Ile Asp Phe Pro Asp Leu Gly Tyr Gly Thr Ala Val Pro Pro Ser
 645 650 655
 Ala Val Phe His Glu Asp Gln Phe Leu Pro Glu Thr Ile Asn Trp Glu

660
 Glu Phe Ala Met Leu Asn Gly Met Asp Thr Met Ser Lys
 675 680 685

<210> 83
 <211> 1239
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 83
 atggtcaaca cccacccgga tcaacggccc cagctctccc cgtccaaccc caatcccccg 60
 tctcgacgac gcaatgatcg cgacatctac gtcgccgatg ccagtgagec cgccacccccg 120
 cgccccatgg acgataccca ccccgccgcc gccaccgccg ccgttgccct ggcccaatta 180
 caccacaatc gcttgggtctc cgactgggag acggacatgg aatcccactc cgacaatgac 240
 atcagccgcg accgcatgcg atcctccatc gagctccctt ctctgcgcga ccacttcaag 300
 caggactccc tcccaccctt ctecccgcgga ccgcgcgaac tgctcccttc catcctcaac 360
 cactcgcccc caggtcgctc ctccactctt cccccatcc agcaaaagaa gtggccgcgc 420
 ccgcgcaaat cctccatctc cggcgctcgc aagcccaaac atgaacgctc caagtccaag 480
 gagtacggtc gccgcccag cttaggcgat cgcaaagccc tgtccgcga accccagacc 540
 gccgcctggg ctcaaggcaa gcgctgggag gatctgatcg aagccgcgac ttcggcgacc 600
 gaggcgcgac acgaacgcca ttctgaggtc ggtcggtcgc ccaccatccc tccggtgtcc 660
 agcttcacct ccgcccccat ggggaagaat cgctcgctgc ttcccccggt attccaagga 720
 ctaccacccc ccacctcgca tgcctcggtt ccgcctcatc cctacgcgcg gtgcgcgttg 780
 aacaacgacc tggagccctt cccctcgata gactcgctcc tcgactccgc ctgcacgcgcg 840
 tccggaaaga cctccacta taatcacgtc ggtccggcca acgactccag tccggtgtctg 900
 aacatgttcc cgtcgtcggc cgtgcagcgc caacaccatc gcttttccaa cccaccccc 960
 gcctccatgc ggagccgcga gatccagatc tattgcgccc actgcaagcg accgtgggcg 1020
 ctcaacgaat gctacgcctg caccgagtcg atctgcggcg tctgtcgcga atgtgtcgga 1080
 atgttcatcg gcagcccgcc cactccttc cgcaacgtca cctccagccc gggcagtgcc 1140
 ttgccccacg gccgaccag ctatcctagc gcccgaggtt gtccccgctg tcgcacgcgc 1200
 ggcggcaagt ggaaggcttt tcagctggat ttcaagtag 1239

<210> 84
 <211> 412
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 84
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 1 5 10 15
 Pro Asn Pro Pro Ser Arg Arg Arg Asn Asp Arg Asp Ile Tyr Val Ala
 20 25 30
 Asp Ala Ser Glu Pro Ala Thr Pro Arg Pro Met Asp Asp Thr His Pro
 35 40 45
 Ala Ala Ala Thr Ala Ala Val Ala Leu Ala Gln Leu His His Asn Arg
 50 55 60
 Leu Val Ser Asp Trp Glu Thr Asp Met Glu Ser His Ser Asp Asn Asp
 65 70 75 80
 Ile Ser Arg Asp Arg Met Arg Ser Ser Ile Glu Leu Pro Ser Leu Arg
 85 90 95

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Asp His Phe Lys Gln Asp Ser Leu Pro Pro Phe Ser Pro Arg Pro Arg
      100      105      110
Glu Leu Leu Pro Ser Ile Leu Asn His Ser Pro Pro Gly Arg Ser Ser
      115      120      125
Thr Leu Pro Pro Ile Gln Gln Lys Lys Trp Pro Arg Pro Arg Lys Ser
      130      135      140
Ser Ile Ser Gly Ala Arg Lys Pro Lys His Glu Arg Ser Lys Ser Lys
      145      150      155      160
Glu Tyr Gly Arg Arg Pro Ser Leu Gly Asp Arg Lys Ala Leu Ser Ala
      165      170      175
Glu Pro Gln Thr Ala Ala Trp Ala Gln Gly Lys Arg Trp Glu Asp Leu
      180      185      190
Ile Glu Ala Ala Thr Ser Ala Thr Glu Ala Asp Asp Glu Arg His Ser
      195      200      205
Glu Val Gly Arg Ser Pro Thr Ile Pro Pro Val Ser Ser Phe Thr Ser
      210      215      220
Ala Pro Met Gly Lys Asn Arg Ser Ser Leu Pro Pro Gly Phe Gln Gly
      225      230      235      240
Leu Pro Pro Pro Thr Ser His Arg Pro Phe Pro Pro His Pro Tyr Ala
      245      250      255
Ala Ser Pro Leu Asn Asn Asp Leu Glu Pro Phe Pro Ser Ile Glu Ser
      260      265      270
Ser Leu Asp Ser Ala Ser Thr Ala Ser Gly Lys Thr Leu His Tyr Asn
      275      280      285
His Val Gly Pro Ala Asn Asp Ser Ser Pro Val Leu Asn Met Phe Pro
      290      295      300
Ser Ser Ala Val Gln Arg Gln His His Arg Phe Ser Asn Pro Thr Pro
      305      310      315      320
Ala Ser Met Arg Ser Arg Glu Ile Gln Ile Tyr Cys Ala His Cys Lys
      325      330      335
Arg Pro Trp Ala Leu Asn Glu Cys Tyr Ala Cys Thr Glu Cys Ile Cys
      340      345      350
Gly Val Cys Arg Glu Cys Val Gly Met Phe Ile Gly Ser Pro Pro Thr
      355      360      365
Ser Phe Arg Asn Val Thr Ser Ser Pro Gly Ser Ala Leu Pro His Gly
      370      375      380
Pro Thr Ser Tyr Pro Ser Ala Arg Gly Cys Pro Arg Cys Arg Thr Val
      385      390      395      400
Gly Gly Lys Trp Lys Ala Phe Gln Leu Asp Phe Lys
      405      410

```

<210> 85
 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

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<400> 85
atgctggaca ttccgaagga catcgagaag atctcgatcc ctgtgagctt tgccttgggc 60
gagcatgaca gcgcaatcaa gccggctcag gtcactcaga tcaagcaaac tctgaatgca 120
aaggaagaga atgtggctag tgaagtgaag atgtattacg gtgttggtca cggcttctgc 180
gtgagagcgg ataccaaact ggtggacgca gacacacaag caactgaggc agagaatcag 240
gccctggctt ggttcaatcg tcatttcgcg gacttttcat cc 282

```

<210> 86
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 86
 Met Leu Asp Ile Pro Lys Asp Ile Glu Lys Ile Ser Ile Pro Val Ser
 1 5 10 15
 Phe Ala Leu Gly Glu His Asp Ser Ala Ile Lys Pro Ala Gln Val Thr
 20 25 30
 Gln Ile Lys Gln Thr Leu Asn Ala Lys Glu Glu Asn Val Ala Ser Glu
 35 40 45
 Val Lys Met Tyr Tyr Gly Val Gly His Gly Phe Cys Val Arg Ala Asp
 50 55 60
 Thr Lys Leu Val Asp Ala Asp Thr Gln Ala Thr Glu Ala Glu Asn Gln
 65 70 75 80
 Ala Leu Ala Trp Phe Asn Arg His Phe Ala Asp Phe Ser Ser
 85 90

<210> 87
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 87
 atgtctagcc aacctctoct ccaaaccgct cggggcaagc gaattgccct cccaaccgca 60
 gtcgaaccca aggtcttctt cgctaacgag cgcaccttcc tctcatggct taacttcacc 120
 gtcactctgg gcggcctagc ggctcggcctc ctcaatttcg gcgaccgcat cggtcgcatac 180
 tccgcagctc tcttcaccat catcgcgatg ggcgcaatga tctacgcctt ggtgacattc 240
 cactggcgcg cgcagagtat ccgtcggcgc ggacagagcg gtatcgatga ccgattcgggt 300
 cctaccatcc tggccattgc cctcctcgcc gccgtcggtt ttaacttcat cttgcggatt 360
 aaggacgggc agatgaac 378

<210> 88
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 88
 Met Ser Ser Gln Pro Leu Leu Gln Thr Ala Pro Gly Lys Arg Ile Ala
 1 5 10 15
 Leu Pro Thr Arg Val Glu Pro Lys Val Phe Phe Ala Asn Glu Arg Thr
 20 25 30
 Phe Leu Ser Trp Leu Asn Phe Thr Val Ile Leu Gly Gly Leu Ala Val
 35 40 45
 Gly Leu Leu Asn Phe Gly Asp Arg Ile Gly Arg Ile Ser Ala Ala Leu
 50 55 60

```

Phe Thr Ile Ile Ala Met Gly Ala Met Ile Tyr Ala Leu Val Thr Phe
65          70          75          80
His Trp Arg Ala Gln Ser Ile Arg Arg Arg Gly Gln Ser Gly Ile Asp
          85          90          95
Asp Arg Phe Gly Pro Thr Ile Leu Ala Ile Ala Leu Leu Ala Ala Val
          100         105         110
Val Val Asn Phe Ile Leu Arg Ile Lys Asp Gly Gln Met Asn
          115         120         125

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<210> 89
 <211> 387
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

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<400> 89
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ctagaggtca cgaactccgg gacgcgagtc cagtgtggga tgacggaagt cggtagcgag 120
acggtctggg atcttgtctt gcttcctacg ccatcgtccc tgcttcaagg gttggcgggc 180
acaggggcgg cttctcgtgg tggctctagc cgctcgtcgc gccctcgtgg gcgacgggat 240
gacgatgagg atacgaggaa agactctgac tcctctgtat tggaatatag tgatgactct 300
tgtgacgatg ggtggacgat tagggcagac cccgttgtga ggcacgaga cggcctggcg 360
catcaggaca ttaccatgcg caaatgc                                     387

```

<210> 90
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

```

<400> 90
Met His Asp Asp Ser Gly Lys Ser Gly Leu Gln Ile Gln Asn Val Glu
1          5          10          15
Thr Gly Gly Trp Leu Glu Val Thr Asn Ser Gly Thr Arg Val Gln Cys
          20          25          30
Gly Met Thr Glu Val Gly Ser Glu Thr Val Trp Asp Leu Val Leu Leu
          35          40          45
Pro Thr Pro Ser Ser Leu Leu Gln Gly Leu Ala Gly Thr Gly Ala Ala
          50          55          60
Ser Arg Gly Gly Ser Ser Arg Ser Ser Arg Pro Arg Gly Arg Arg Asp
65          70          75          80
Asp Asp Glu Asp Thr Arg Lys Asp Ser Asp Ser Ser Val Leu Glu Tyr
          85          90          95
Ser Asp Asp Ser Cys Asp Asp Gly Trp Thr Ile Arg Ala Asp Pro Val
          100         105         110
Val Arg His Arg Asp Gly Leu Ala His Gln Asp Ile Thr Met Arg Lys
          115         120         125
Cys

```

<210> 91

<211> 2274

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 91

```

atgatctccg ctccgggtcc cgagcgacgg cgcagacggc cggcagtgtc atgttctctt 60
tgcagaaggc gtaagattaa atgcaaccgc gaaagccctt gtagcaactg catcaagtct 120
aaggcggaac catgcgctta cgagagcgac tcctcgctcc ggccgcagca gcatcttggc 180
ttcaatcaga cactggagct agggctctgc aaggcgctctg aacgccagat gctccctcca 240
gatgcggtaa cttctcaagt tcctagctat gcgtccagggt cattactctc cagcgcgaga 300
gactcgctcat cccggacgag tcaagcttct gcatcggagg ttgagtctct gaagaccaag 360
atcagacagc tggaggaaca gctgtccagt gcgacgcagc cggcggaatc acctccacgg 420
ccgtctccaa actccagaat cgagaccagc acgtctcaga tagcaggagc gttccacata 480
aaccatgaaa ggcggcttct ccacgattcc cagttcgtea accgaaatct ggtcatacat 540
aaaagtcgcc tgtttggtct cagtcattgg gcacaggctg catcgatgtt tagagatgta 600
tttgaaatga tcgaaccggt tatccgcggg agtggttcca aagccagtgc cggcatcaga 660
aggtgcaaag agctggcaag gattatcaaa acccaacgga cgccgcaatg gccgacgccg 720
cccactcagg atctacctcc aaaaggcgtc gctgatgagt tggttgactg ctatctccgt 780
acaatcgaga ctacattccg ggtcctgcac gtacctacat tcagggtccg atatgacgct 840
ctatgggtat ctgaagcacg gccagcatc gcgttcacag tccaacttaa gctggtgttg 900
gcactggggt ctgtcaacta cgacgagcgg ttttcaatga gaccagtgct ggttcggttg 960
gtatttgagg cgcacacctg gctctctgat ccagacttca aacctcaact taacatacag 1020
tgtttgcaaa gcaggattct actattacta gcccgcgaga taatcaatgt tggtggcgat 1080
tcgagttgga tatctgccgg cggactactc cgcactgctc tacatatggg attacatagg 1140
gatccgtctg tactgccgcc taggtcggcg ctgctgtttg aaatgcgacg ccgactgtgg 1200
aacactatcc tcgagctatc actgcagtca agcatttccct ccggtggacc tccactaatt 1260
tccttgggag atttcgactg tgcgcctcca gggaatttctg acgacgaaca gctactggct 1320
gaggaccgag tgccgaagag tgatgatgag tacactcaaa cagcaatcgc cagggcattg 1380
aggggaacct acccacagcg ccttgcaatt gtgaaattcc tgaacgatct aagttcatat 1440
gggacttacg aggaaactct tcgacttgac gcagatttaa gggaatctta cagggtctatt 1500
tgccgtatcc tccgagggtg tcccagcaac gggccttccc cgtcacagtt cgaaaaatgc 1560
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tactgcggg caccggcata tgcattctcc aggaaagtcg cgatcgagag cgccctcaag 1680
atgtggtgcg ccatttacct atcttccaga ttcattgagc acaccgctcg cgagattagc 1740
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ggtgttataa tcgcggccat gttcgtgacc ttggagctta aagctcagct cctggatgat 1860
gacagcctag gtcccagccc gtatcgggta gatcttttct ctctgctctg tgaggcgaaa 1920
gaccgttggt ggaatatgat tcaatgtggt gagactaatg tcaagggtta cctcctcatt 1980
tgtctggtaa ccgccagat cgaggggctg atgcatggag ttgaaccgag caaactcccc 2040
gaactccttc tccgcgcagc agaagaggcg gaggaccggt gtcttgactt catggaggag 2100
aaagccgagc tgggacggag tgggtggttc gttgaggtga tggacgaatc tgcgaataca 2160
gcgcccttca tgggcgactg ggagtttatt atgacagatc ctttccttaa ttatcctggg 2220
actactgaac cactcagctg ggttatgaat gaagaaacga gaccattcat aatg 2274

```

<210> 92

<211> 758

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 92

Met Ile Ser Ala Pro Gly Pro Glu Arg Arg Arg Arg Pro Ala Val

1				5					10				15				
Ser	Cys	Ser	Leu	Cys	Arg	Arg	Arg	Lys	Ile	Lys	Cys	Asn	Arg	Glu	Ser		
			20					25					30				
Pro	Cys	Ser	Asn	Cys	Ile	Lys	Ser	Lys	Ala	Glu	Pro	Cys	Val	Tyr	Glu		
		35					40					45					
Ser	Asp	Ser	Ser	Ser	Arg	Pro	Gln	Gln	His	Leu	Gly	Phe	Asn	Gln	Thr		
	50				55					60							
Leu	Glu	Leu	Gly	Leu	Cys	Lys	Ala	Ser	Glu	Arg	Gln	Met	Leu	Pro	Pro		
65				70					75						80		
Asp	Ala	Val	Thr	Ser	Gln	Val	Pro	Ser	Tyr	Ala	Ser	Arg	Ser	Leu	Leu		
				85					90					95			
Ser	Ser	Ala	Arg	Asp	Ser	Ser	Ser	Arg	Thr	Ser	Gln	Ala	Ser	Ala	Ser		
			100					105						110			
Glu	Val	Glu	Ser	Leu	Lys	Thr	Lys	Ile	Arg	Gln	Leu	Glu	Glu	Gln	Leu		
		115					120					125					
Ser	Ser	Ala	Thr	Gln	Pro	Ala	Glu	Ser	Pro	Pro	Arg	Pro	Ser	Pro	Asn		
	130					135					140						
Ser	Arg	Ile	Glu	Thr	Ser	Thr	Ser	Gln	Ile	Ala	Gly	Thr	Phe	His	Ile		
145					150				155						160		
Asn	His	Glu	Arg	Arg	Leu	Leu	His	Asp	Ser	Gln	Phe	Val	Asn	Arg	Asn		
				165				170						175			
Leu	Val	Ile	His	Lys	Ser	Arg	Leu	Phe	Gly	Ser	Ser	His	Trp	Ala	Gln		
			180					185					190				
Ala	Ala	Ser	Met	Phe	Arg	Asp	Val	Phe	Glu	Met	Ile	Glu	Pro	Phe	Ile		
		195					200				205						
Arg	Gly	Ser	Gly	Ser	Lys	Ala	Ser	Ala	Gly	Ile	Arg	Arg	Cys	Lys	Glu		
	210				215						220						
Leu	Ala	Arg	Ile	Ile	Lys	Thr	Gln	Arg	Thr	Pro	Gln	Trp	Pro	Thr	Pro		
225					230					235					240		
Pro	Thr	Gln	Asp	Leu	Pro	Pro	Lys	Gly	Val	Ala	Asp	Glu	Leu	Val	Asp		
				245				250						255			
Cys	Tyr	Leu	Arg	Thr	Ile	Glu	Thr	Thr	Phe	Arg	Val	Leu	His	Val	Pro		
			260					265					270				
Thr	Phe	Arg	Ser	Glu	Tyr	Asp	Ala	Leu	Trp	Val	Ser	Glu	Ala	Arg	Pro		
		275					280					285					
Ser	Ile	Ala	Phe	Thr	Val	Gln	Leu	Lys	Leu	Val	Leu	Ala	Leu	Gly	Ser		
	290					295					300						
Val	Thr	Tyr	Asp	Glu	Arg	Phe	Ser	Met	Arg	Pro	Ser	Ala	Val	Arg	Trp		
305					310					315					320		
Val	Phe	Glu	Ala	His	Thr	Trp	Leu	Ser	Asp	Pro	Asp	Phe	Lys	Pro	Gln		
				325					330					335			
Leu	Asn	Ile	Gln	Cys	Leu	Gln	Ser	Arg	Ile	Leu	Leu	Leu	Leu	Ala	Arg		
			340					345					350				
Glu	Ile	Ile	Asn	Val	Gly	Gly	Asp	Ser	Ser	Trp	Ile	Ser	Ala	Gly	Gly		
		355					360					365					
Leu	Leu	Arg	Thr	Ala	Leu	His	Met	Gly	Leu	His	Arg	Asp	Pro	Ser	Val		
	370					375					380						
Leu	Pro	Pro	Arg	Ser	Ala	Leu	Ala	Val	Glu	Met	Arg	Arg	Arg	Leu	Trp		
385					390					395					400		
Asn	Thr	Ile	Leu	Glu	Leu	Ser	Leu	Gln	Ser	Ser	Ile	Ser	Ser	Gly	Gly		
				405				410						415			
Pro	Pro	Leu	Ile	Ser	Leu	Gly	Asp	Phe	Asp	Cys	Ala	Pro	Pro	Gly	Asn		
			420					425					430				
Phe	Asp	Asp	Glu	Gln	Leu	Leu	Ala	Glu	Asp	Pro	Val	Pro	Lys	Ser	Asp		
		435					440					445					
Asp	Glu	Tyr	Thr	Gln	Thr	Ala	Ile	Ala	Arg	Ala	Leu	Arg	Gly	Thr	Tyr		
	450					455					460						


```

Pro Gln Arg Leu Ala Ile Val Lys Phe Leu Asn Asp Leu Ser Ser Tyr
465                               470           475           480
Gly Thr Tyr Glu Glu Thr Leu Arg Leu Asp Ala Asp Leu Arg Glu Ser
                               485           490           495
Tyr Arg Ala Ile Cys Arg Ile Leu Arg Gly Tyr Pro Ser Asn Gly Pro
                               500           505           510
Ser Pro Ser Gln Phe Glu Lys Cys Met Leu Asp Phe Ile Ile His Phe
                               515           520           525
Tyr Val Cys Cys Leu His Ile Pro Tyr Ile Glu Lys Ser Leu Arg Ala
530                               535           540
Pro Ala Tyr Ala Phe Ser Arg Lys Val Ala Ile Glu Ser Ala Leu Lys
545                               550           555           560
Met Trp Cys Ala Ile Tyr Pro Ser Ser Arg Phe Met Ser Asn Thr Arg
                               565           570           575
Arg Glu Ile Ser Gly Ser Val Glu Asn Lys Leu Thr Arg Phe Val Glu
                               580           585           590
Cys Gly Phe Gly Phe Phe Arg Thr Gly Val Ile Ile Ala Ala Met Phe
                               595           600           605
Val Thr Leu Glu Leu Lys Ala Gln Leu Leu Asp Asp Asp Ser Leu Gly
610                               615           620
Pro Ser Pro Tyr Arg Val Asp Leu Phe Ser Leu Leu Cys Glu Ala Lys
625                               630           635           640
Asp Arg Cys Trp Asn Met Ile Gln Cys Gly Glu Thr Asn Val Lys Gly
                               645           650           655
Tyr Leu Leu Ile Cys Leu Val Thr Ala Gln Ile Glu Gly Leu Met His
                               660           665           670
Gly Val Glu Pro Ser Lys Leu Pro Glu Leu Leu Leu Arg Ala Ala Glu
                               675           680           685
Glu Ala Glu Asp Arg Cys Leu Asp Phe Met Glu Glu Lys Ala Asp Leu
690                               695           700
Gly Arg Ser Gly Gly Ser Val Glu Val Met Asp Glu Ser Ala Asn Thr
705                               710           715           720
Ala Pro Phe Met Gly Asp Trp Glu Phe Ile Met Thr Asp Pro Phe Leu
                               725           730           735
Asn Tyr Pro Gly Thr Thr Glu Pro Leu Ser Trp Val Met Asn Glu Glu
740                               745           750
Thr Arg Pro Phe Ile Met
755

```

<210> 93

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 93

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atgaccagca caatagcccg cactgaggaa cgccagaacg ctggcaccat tgaactgaaa 60
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cctgcactgt tcggtcttta cgtaacaaa ttcctcccca aggggatcaa gatcgtcgga 180
tatgctcgga cgaacatgga ccacgaagaa tatctgagac ggggtgcgctc gtacatcaag 240
acccccacca aggaaatcga agaacagctg gatggcttct gccagctgtg cacctacatc 300
agcggccaat atgacaagga tgactcgttc attaacctca ctaagcacct cgaggacgtc 360
gagaagggcc ataaggaaca gaacagagtc ttctacatgg cgctgcctcc tagcgtcttc 420
attaccgtgt cggatcaatt gaagagaaac tgctacccca agaacggcat tgcccgtatt 480

```

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attgtcgaga agcccttcgg caaggatctc cagagttctc gtgacctcca gaaggccctt 540
gagcccaact ggaaagagga ggagatcttc cgtattgacc actacctggg taaggagatg 600
gtcaagaaca tcctcatcat gcgcttcgga aacgagttct tcaacgctac ctggaaccgt 660
caccacattg ataacgtgca gatcacattc aaggagccgt tcggcacgga gggccgtgga 720
ggctactttg atgagttcgg catcattcgt gatgtcatgc agaaccacct tctgcagggtg 780
ttgacgcttc ttgccatgga gcgtcccatc tctttctctg ctgaagacat tctgacgag 840
aaggtgcgtg ttctgcgcgc gatggacccc attgagccca agaacgtcat catcgccag 900
tacggaagt cgctcgacgg tagcaagccc gcctacaagg aggatgatac tgtgcctcaa 960
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atccagttcc gtgacgtcac ttccggcatc ttcaaggaca tccccgcaa cgaacttgctc 1140
attcgtgtcc agcccaacga gtcgggtgtac attaatgatga actcgaagct accgggtctc 1200
tccatgcaga cggtcgttac cgagcttgac cttacctacc gccgcccgtt ctccgacctc 1260
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tttgtccgtg acgatgaact tgactcgagc ttgaagatct tcacctctct gctgcactac 1380
ctggacgaca acaaggagat tatccccatg gaatacccct acggctctcg cggacctgct 1440
gtgctcgacg acttcaccgc gtcgttcggg tacaagttca gtgatgctgc tggctaccag 1500
tggcccctga cttcggctcc caacagactg 1530

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<210> 94

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 94

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Met Thr Ser Thr Ile Ala Arg Thr Glu Glu Arg Gln Asn Ala Gly Thr
  1          5          10          15
Ile Glu Leu Lys Asp Asp Thr Val Ile Val Val Leu Gly Ala Ser Gly
  20          25          30
Asp Leu Ala Lys Lys Lys Thr Phe Pro Ala Leu Phe Gly Leu Tyr Arg
  35          40          45
Asn Lys Phe Leu Pro Lys Gly Ile Lys Ile Val Gly Tyr Ala Arg Thr
  50          55          60
Asn Met Asp His Glu Glu Tyr Leu Arg Arg Val Arg Ser Tyr Ile Lys
  65          70          75          80
Thr Pro Thr Lys Glu Ile Glu Glu Gln Leu Asp Gly Phe Cys Gln Leu
  85          90          95
Cys Thr Tyr Ile Ser Gly Gln Tyr Asp Lys Asp Asp Ser Phe Ile Asn
  100         105         110
Leu Thr Lys His Leu Glu Asp Val Glu Lys Gly His Lys Glu Gln Asn
  115         120         125
Arg Val Phe Tyr Met Ala Leu Pro Pro Ser Val Phe Ile Thr Val Ser
  130         135         140
Asp Gln Leu Lys Arg Asn Cys Tyr Pro Lys Asn Gly Ile Ala Arg Ile
  145         150         155         160
Ile Val Glu Lys Pro Phe Gly Lys Asp Leu Gln Ser Ser Arg Asp Leu
  165         170         175
Gln Lys Ala Leu Glu Pro Asn Trp Lys Glu Glu Glu Ile Phe Arg Ile
  180         185         190
Asp His Tyr Leu Gly Lys Glu Met Val Lys Asn Ile Leu Ile Met Arg
  195         200         205
Phe Gly Asn Glu Phe Phe Asn Ala Thr Trp Asn Arg His His Ile Asp
  210         215         220
Asn Val Gln Ile Thr Phe Lys Glu Pro Phe Gly Thr Glu Gly Arg Gly

```

225					230					235				240
Gly	Tyr	Phe	Asp	Glu	Phe	Gly	Ile	Ile	Arg	Asp	Val	Met	Gln	Asn
				245					250				255	
Leu	Leu	Gln	Val	Leu	Thr	Leu	Leu	Ala	Met	Glu	Arg	Pro	Ile	Ser
			260					265					270	
Ser	Ala	Glu	Asp	Ile	Arg	Asp	Glu	Lys	Val	Arg	Val	Leu	Arg	Ala
		275					280					285		
Asp	Pro	Ile	Glu	Pro	Lys	Asn	Val	Ile	Ile	Gly	Gln	Tyr	Gly	Lys
	290					295					300			
Leu	Asp	Gly	Ser	Lys	Pro	Ala	Tyr	Lys	Glu	Asp	Asp	Thr	Val	Pro
305					310					315				Gln
Asp	Ser	Arg	Cys	Pro	Thr	Phe	Cys	Ala	Met	Val	Ala	Tyr	Ile	Lys
			325						330					335
Glu	Arg	Trp	Asp	Gly	Val	Pro	Phe	Ile	Met	Lys	Ala	Gly	Lys	Ala
			340					345					350	
Asn	Glu	Gln	Lys	Thr	Glu	Ile	Arg	Ile	Gln	Phe	Arg	Asp	Val	Thr
	355						360					365		Ser
Gly	Ile	Phe	Lys	Asp	Ile	Pro	Arg	Asn	Glu	Leu	Val	Ile	Arg	Val
	370					375					380			Gln
Pro	Asn	Glu	Ser	Val	Tyr	Ile	Lys	Met	Asn	Ser	Lys	Leu	Pro	Gly
385					390					395				Leu
Ser	Met	Gln	Thr	Val	Val	Thr	Glu	Leu	Asp	Leu	Thr	Tyr	Arg	Arg
			405					410					415	
Phe	Ser	Asp	Leu	Lys	Ile	Pro	Glu	Ala	Tyr	Glu	Ser	Leu	Ile	Leu
		420					425					430		Asp
Ala	Leu	Lys	Gly	Asp	His	Ser	Asn	Phe	Val	Arg	Asp	Asp	Glu	Leu
	435					440					445			Asp
Ser	Ser	Trp	Lys	Ile	Phe	Thr	Pro	Leu	Leu	His	Tyr	Leu	Asp	Asp
	450				455					460				Asn
Lys	Glu	Ile	Ile	Pro	Met	Glu	Tyr	Pro	Tyr	Gly	Ser	Arg	Gly	Pro
465				470					475					Ala
Val	Leu	Asp	Asp	Phe	Thr	Ala	Ser	Phe	Gly	Tyr	Lys	Phe	Ser	Asp
			485					490					495	
Ala	Gly	Tyr	Gln	Trp	Pro	Leu	Thr	Ser	Ala	Pro	Asn	Arg	Leu	
		500						505					510	

<210> 95

<211> 2550

<212> DNA

<213> Artificial Sequence.

<220>

<223> fungal gene

<400> 95

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agaaaaactca aatgcaaccg tgctcatcca tgtgaaaact gcgtcaaacg gggcgatgcc 180
tcgtcctgta cctatgcaca agccaacgag cggaaaaaga actcaccgct tcagaccgct 240
tcgagctcac ccgacgacat gcaaaaccgg atagatcgtc ttgagagctt ggtgctctct 300
ttgatgacca atggatctca gtccgcaggc cccacggcag ctatggcggt catttccggc 360
aactccagca gcatcggtct cgctcaacat acgtcggaag atgtagagct ggacgatgat 420
gatgggcaag gtcccaggga gactgatacg gagcaattga ccaagtcgat cggtatcatg 480
aaggctcgaca acaacaaatc gtggtatatc agtgatgcac attgggcatc ggtcctgagc 540
gatatagcgg aagtcaaaaa ttacttcaac acgcacaaga agcaatatga agaacacgca 600
gagaaaatta aagcgacgag actcccaaca gatgttcccg gctcgacctt gctcttcggt 660

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gggacgaaaa cgataagtcg cgaggaaatc atggcctctt tcccatccag gtatactgcg 720
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cctaccctttc aggcgcagta caataaacac tgggaggacc cctccaaaac ctgtattggt 840
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acacagggcg gaattgcagg aaggatgcgt acgatgccgt cgctttctag cgcattccca 2460
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<210> 96

<211> 850

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 96

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Met Thr Pro Thr Pro Pro Ser Thr Thr Ser Ser Ser Ala Gly Gly Ile
 1              5              10              15
Ser Pro Glu Gly His Tyr Arg Val Ile Arg Lys Arg Asn Arg Val Pro
              20              25              30
Leu Ser Cys Gly Pro Cys Arg His Arg Lys Leu Lys Cys Asn Arg Ala
              35              40              45
His Pro Cys Glu Asn Cys Val Lys Arg Gly Asp Ala Ser Ser Cys Thr
              50              55              60
Tyr Ala Gln Ala Asn Ala Arg Lys Lys Asn Ser Pro Leu Gln Thr Ala
65              70              75              80
Ser Ser Ser Pro Asp Asp Met Gln Asn Arg Ile Asp Arg Leu Glu Ser
              85              90              95
Leu Val Leu Ser Leu Met Thr Asn Gly Ser Gln Ser Ala Gly Pro Thr
              100              105              110
Ala Ala Met Ala Val Ile Ser Gly Asn Ser Ser Ser Ile Gly Ser Ala

```


Pro Asn Gly Arg Leu Arg Gly Lys Leu Asn Arg Thr Thr Ser Leu Cys
 580 585 590
 Ser Ser Asp Phe Leu Leu Ala Ala Thr Ile Val Cys Leu Asp Leu Tyr
 595 600 605
 His Gly Leu Gln Leu Gln Ala Gly Gly Arg Ala Ser Asp Asp Thr Tyr
 610 615 620
 Thr Trp Gly Arg Glu Arg Arg Asp Glu Met Val Ala Ala Leu Gln Arg
 625 630 635 640
 Ser Lys Glu Ile Trp Asp Glu Leu Gln Asp Glu Thr Ile Asp Ala Trp
 645 650 655
 Lys Ala Ser Gly Val Leu Gly Val Met Leu Ala Arg Leu Asn Leu Asp
 660 665 670
 Gly Asn Thr Ala Ser Thr Thr Phe Glu Pro Gln Asp Glu Lys Gln Ser
 675 680 685
 Ala Ala Met Thr Leu Gly Leu Leu Ser Ser Gly Met Asn Tyr Met Asn
 690 695 700
 Pro Gly Thr Pro Gly Phe Gly Glu Ala Thr Thr Lys Met Ala Asp Thr
 705 710 715 720
 Pro Val Pro Pro Pro Gly Gly Phe Gly Ala Ala Asp Met Pro Gly Ala
 725 730 735
 Pro Ser Pro Phe Ser Ala Met Phe Gly Gln Met Pro Asp Met Gln Val
 740 745 750
 Asn Leu Asp Trp Asp Ala Trp Asp Asn Tyr Ile Gln Asn Ser Ser Ile
 755 760 765
 Asp Phe Ser Asn Gln Trp Trp Pro Ala Met Asp Ala Gln Gln Ala Pro
 770 775 780
 Gln Pro Pro Gln Pro Gly Asn Pro Leu Ser Pro Ser Gln Leu Ala Ala
 785 790 795 800
 Thr Gln Gly Gly Ile Ala Gly Arg Met Arg Thr Met Pro Ser Leu Ser
 805 810 815
 Ser Ala Phe Pro Glu Pro Asn Gly Tyr Asp Ala Ala Phe Pro Thr Ser
 820 825 830
 Phe Ser Val Asn Ala Pro Lys Asn Pro His Asn Pro Ala Ser Gly Pro
 835 840 845
 Gly Thr
 850

<210> 97

<211> 927

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 97

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 ccgtgcggcc ggtgtcgcgc agacaatgcc atctgcgtct ttggcgagcg caaaaaggcg 180
 catgacaaag tgtaccccaa gggatacggt gagatgcttg aacagcagca ggcctggctc 240
 gtctacggcc tgcaggaaact gtaccgcccgc accagcgacg gcgaaggctg gcccggcgag 300
 ccgtcaagt gcgaggccaa cgccacccg ctcacgcacg acctgtcac ccgcctcggc 360
 gccctcgacc aggccaaagg cgagcgcttc gaggaaaacc ccgacgcat gcagcaggag 420
 ctctggcgcc agaacgccg ccacatgcag cgccaggact cgtccgacgc cagctccgac 480
 agcgcccaact cgcccgtcgt cccctccgtc gccgcccgcg ccgcccgtcg ctccgcccag 540
 cccttcgccc agccccagct gccccccacc ccgcaaaata tcagccccag cgcccgcgcc 600

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gtcaagtccg agtcgtcgca gatgccgccg gcctttgcgt ccgcgccgct gggcatgcag 660
ggcgtcgtca accccatggg gctgcaggcg ccgcagcagc aacagcagca gcagcagtcg 720
tggggaggga atgggttcgg cgggttcgat gatatcgaca tgatgggcac gacggatttt 780
accaacctgt cgtttgacga tccgctgtcg tcgccgatgt tcaatcgacc cgtgccgata 840
aactgcatgt cgtatatgga cttgaaggcg gactacgacg atctgaacca gtttgtcaat 900
gcgaatgcgc cggagatcgc gtcgacg                                     927

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<210> 98

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 98

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Met Thr Pro Arg Gln Ser Ser Pro Ser Glu His Ser His Ser Asp Asn
 1          5          10          15
Asn Val Arg Lys Arg Val Cys Lys Ala Cys Asp Arg Cys Arg Leu Lys
      20          25          30
Lys Ser Lys Cys Asp Gly Gly Asn Pro Cys Gly Arg Cys Arg Ala Asp
      35          40          45
Asn Ala Ile Cys Val Phe Gly Glu Arg Lys Lys Ala His Asp Lys Val
      50          55          60
Tyr Pro Lys Gly Tyr Val Glu Met Leu Glu Gln Gln Gln Ala Trp Leu
      65          70          75          80
Val Tyr Gly Leu Gln Glu Leu Tyr Arg Arg Thr Ser Asp Gly Glu Gly
      85          90          95
Trp Pro Gly Glu Pro Leu Lys Cys Glu Ala Asn Gly His Pro Leu Thr
      100         105         110
His Asp Leu Leu Thr Arg Leu Gly Ala Leu Asp Gln Ala Lys Gly Glu
      115         120         125
Arg Phe Glu Glu Asn Pro Asp Ala Met Gln Gln Glu Leu Trp Arg Gln
      130         135         140
Asn Ala Gly His Met Gln Arg Gln Asp Ser Ser Asp Ala Ser Ser Asp
      145         150         155         160
Ser Ala His Ser Pro Val Val Pro Ser Val Ala Ala Ala Ala Ala Ala
      165         170         175
Arg Phe Ala Asp Pro Phe Ala Gln Pro Gln Leu Pro Pro Thr Pro Pro
      180         185         190
Asn Ile Ser Pro Ser Ala Arg Pro Val Lys Ser Glu Ser Ser Gln Met
      195         200         205
Pro Pro Ala Phe Ala Ser Ala Pro Leu Gly Met Gln Gly Val Val Asn
      210         215         220
Pro Met Val Leu Gln Ala Pro Gln Gln Gln Gln Gln Gln Gln Gln Ser
      225         230         235         240
Trp Gly Gly Asn Gly Phe Gly Gly Phe Asp Asp Ile Asp Met Met Gly
      245         250         255
Thr Thr Asp Phe Thr Asn Leu Ser Phe Asp Asp Pro Leu Ser Ser Pro
      260         265         270
Met Phe Asn Arg Pro Val Pro Ile Asn Cys Met Ser Tyr Met Asp Leu
      275         280         285
Lys Gly Asp Tyr Asp Asp Leu Asn Gln Phe Val Asn Ala Asn Ala Pro
      290         295         300
Glu Ile Ala Ser Thr
305

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<210> 99
 <211> 1374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 99
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 gtgaacctgc ctcggtttca cccaatcgcc atgaaccgga gccagccagt ccatccagag 180
 cacatggccg tgccaaatca tctcactttt cgcccatttc cgccgcccgc gccaatgcat 240
 gaacccgggc cgcctcccc gggtgtcat cccgccata tagatcatat cgaagctcga 300
 ctgaggcagt tggagcatga ggaagccgct cgcattggcg ctctagtca actactcga 360
 atccgcaagc ggaagacga agaattccgt aggatgaccg agaacgctga agcgggaagaa 420
 gaggaactac gtagacagcg gaaacgcctg aagcgcgagt ccatgggtct ggggttcaat 480
 gccaccgttg actcgctcc cctacgtccc acgcgcctc gccggtatc agaaacaaac 540
 gcagccacca ctctggcctt cttcaagcaa caaagcccgc cagagccacg accgattccc 600
 gtgcaggcgc cgcgcacca cccgccaccg cctccgcagc atctgcacga ctgcacgggg 660
 gccaccatcc gccgcaagca gaaatacacg atcaaaaacg tcgaagcatg gggcgagcgc 720
 cagggcgtc ccgcggcgca cgaccgtcc ggccgcgcgc tgtggaagcg gccctccgac 780
 ggcagccttg tgtacctac ctgcccgtg tcgggctgcg gcaaggccga ctttgtcacg 840
 ctgcacgggt tcatgtgcca tctgaccaag aagcacaagg accgcagcct gggcagccag 900
 tcgcgcgcgc tgaagtctg cggcatcgtc tacgaccca acgcgcgct gccgcccgtg 960
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 tatccgcagg agatggacac gtcttcggta tcggacgagg agcagcgca gcacaccgtc 1080
 aagaccgagt ccaccgagag atcggtgccc gcgcacgcgg cgcccttccc gccccccgac 1140
 gagcccgta aagcatccc tctcaacggc tccacgaaac agaccatctc gtccatcatc 1200
 gaccgcgagc cggacgatga gccgcgcgag cggccgcct ccattcccc cgtccagccc 1260
 gagtcggccg tctgccttc cccggagcag aagtcggctg ttcgggagga ggagcccaag 1320
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<210> 100
 <211> 458
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 100
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 1 5 10 15
 His Glu Asn Gly Leu Asn Gly His Val Pro His Gln His His His His
 20 25 30
 His His His Pro His Gln Thr Asn Val Asn Leu Pro Arg Phe His Pro
 35 40 45
 Ile Ala Met Asn Pro Ser Gln Pro Val His Pro Glu His Met Ala Val
 50 55 60
 Pro Asn His Pro His Phe Arg Pro Phe Pro Pro Pro Pro Met His
 65 70 75 80
 Glu Pro Gly Pro Pro Pro Pro Gly Ala His Pro Ala His Ile Asp His
 85 90 95
 Ile Glu Ala Arg Leu Arg Gln Leu Glu His Glu Glu Ala Ala Arg Met
 100 105 110

Ala Ala Arg Ser Gln Leu Leu Ala Ile Arg Lys Arg Glu Asp Glu Glu
 115 120 125
 Phe Arg Arg Met Thr Glu Asn Ala Glu Ala Glu Glu Glu Glu Leu Arg
 130 135 140
 Arg Gln Arg Lys Arg Leu Lys Arg Glu Ser Met Gly Leu Gly Phe Asn
 145 150 155 160
 Ala Thr Val Asp Ser Pro Pro Leu Arg Pro Thr Pro Pro Arg Arg Leu
 165 170 175
 Ser Glu Thr Asn Ala Ala Thr Thr Leu Ala Phe Phe Lys Gln Gln Ser
 180 185 190
 Pro Pro Glu Pro Arg Pro Ile Pro Val Gln Ala Pro Pro His His Pro
 195 200 205
 Pro Pro Pro Pro Gln His Leu His Asp Ser Thr Gly Ala Thr Ile Arg
 210 215 220
 Arg Lys Gln Lys Tyr Thr Ile Lys Asn Val Glu Ala Trp Gly Glu Arg
 225 230 235 240
 His Gly Arg Pro Ala Ala His Asp Pro Ser Gly Arg Ala Leu Trp Lys
 245 250 255
 Arg Pro Ser Asp Gly Ser Leu Val Tyr Leu Thr Cys Pro Val Ser Gly
 260 265 270
 Cys Gly Lys Ala Asp Phe Val Thr Leu His Gly Phe Met Cys His Leu
 275 280 285
 Thr Lys Lys His Lys Asp Arg Ser Leu Gly Ser Gln Ser Arg Ala Leu
 290 295 300
 Glu Val Cys Gly Ile Val Tyr Asp Pro Asn Ala Pro Leu Pro Pro Val
 305 310 315 320
 Ala Ala Val Pro Arg Ala Ser Thr Glu Glu Ser Arg Leu Glu Ser Pro
 325 330 335
 His Pro Asp Gly Tyr Pro Gln Glu Met Asp Thr Ser Ser Val Ser Asp
 340 345 350
 Glu Glu Gln Arg Glu His Thr Val Lys Thr Glu Ser Thr Glu Arg Ser
 355 360 365
 Leu Pro Ala His Ala Ala Pro Phe Pro Pro Pro Asp Glu Pro Val Lys
 370 375 380
 Ala Ser Arg Leu Asn Gly Ser Thr Lys Gln Thr Ile Ser Ser Ile Ile
 385 390 395 400
 Asp Arg Glu Pro Asp Asp Glu Pro Arg Glu Arg Pro Ala Ser Ile Pro
 405 410 415
 Pro Val Gln Pro Glu Ser Ala Val Leu Pro Ser Pro Glu Gln Lys Ser
 420 425 430
 Val Val Arg Glu Glu Glu Pro Lys Ser Ala Asp Ser Glu Lys Glu Asn
 435 440 445
 Thr Glu Pro Lys Asp Val Ser Glu Thr Lys
 450 455

<210> 101

<211> 1728

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 101

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 ctgttggcct gtcttctgtg ccgtcacaaa cacctcaaat gtgatgggaa aactccagt 120

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tgcggacgct gtgccgtac tggatcggaa tgccaatata ccccgtcgcg tcgtgggtac 180
aagggcccgt cgaagaagcg acgcgcaaac ccgtcgtctc cagagcaaac gcccgccgat 240
ctggccgcct cgttcgatcc gcagtcctac ggtttggtea atgtcaccac tgactggagc 300
ctgcaaaaca cgggtcccttt catgcccgtc gctacottcc cgtcctcctc gtcgaccagc 360
ccgggcttga ccgactacac caattcttcg caacccatcc ggttcacgaa tgacccccta 420
actcccgaact cttccgcctc ggtccccggt gatgggtatt tgatcgatat ctactatacc 480
tatttccatc cctcgcaccc aattctccct ccgctccgct ttctctaccg ctctatatctc 540
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agcgagacgt atcgacccac cgttgtgtca aatgtgaagg agcaagaggg ctctatagag 660
aagctgcagg ctctcttgtt gctcgcggtg gtccctccact ctcgcaatga acgtcccga 720
gctggcgagt gtctcgccgg agctgttgac ctacggtttg agctgggact ccagacgcag 780
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ttcaaatccc tggcccgcac gtgggccatc tcccagacaa tcatgaggca gatcaaagcc 1620
gtgtcgcgcg atgttatgga catgggactg cggccggcca tggaccagat tgatctgacg 1680
accctcctcg atagcggtcg gttcttgatg cccgatggac tgatgcga 1728

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<210> 102

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 102

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Met Asn Asp Pro Phe Val Pro Ala Lys Asn Pro Gly Pro Thr Lys Ala
1      5      10      15
Ala Gly Pro Ser Leu Leu Ala Cys Leu Leu Cys Arg His Lys His Leu
20     25     30
Lys Cys Asp Gly Lys Thr Pro Val Cys Gly Arg Cys Ala Ala Thr Gly
35     40     45
Ser Glu Cys Gln Tyr Thr Pro Ser Arg Arg Gly Tyr Lys Gly Pro Ser
50     55     60
Lys Lys Arg Arg Ala Asn Pro Ser Ser Pro Glu Gln Thr Pro Ala Asp
65     70     75     80
Leu Ala Ala Ser Phe Asp Pro Gln Ser Ile Gly Leu Val Asn Val Thr
85     90     95
Pro Asp Trp Ser Leu Gln Asn Thr Val Pro Phe Met Pro Val Ala Thr
100    105    110
Phe Pro Ser Ser Ser Ser Thr Ser Pro Gly Leu Thr Asp Tyr Thr Asn
115    120    125
Ser Ser Gln Pro Ile Arg Phe Thr Asn Asp Pro Leu Thr Pro Asp Ser
130    135    140
Ser Ala Ser Val Pro Gly Asp Gly Tyr Leu Ile Asp Ile Tyr Tyr Thr
145    150    155    160

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Tyr Phe His Pro Ser His Pro Ile Leu Pro Pro Leu Arg Phe Leu Tyr
      165      170      175
Arg Ser Tyr Leu Pro Thr Phe Leu Glu Gln Val Ile Lys Phe Ile Gly
      180      185      190
Ala His Phe Thr Pro Ala Ala Ser Ser Glu Thr Tyr Arg Pro Thr Val
      195      200      205
Val Ser Asn Val Lys Glu Gln Glu Gly Ser Ile Glu Lys Leu Gln Ala
      210      215      220
Leu Leu Leu Leu Ala Val Val Leu His Ser Arg Asn Glu Arg Pro Glu
      225      230      235      240
Ala Gly Glu Cys Leu Ala Gly Ala Val Asp Leu Ala Phe Glu Leu Gly
      245      250      255
Leu Gln Thr Gln Ser Phe Ala Thr Ala Met Ser Asp Gly Asp Pro Ile
      260      265      270
Arg Ala Glu Cys Leu Arg Arg Thr Trp Trp Glu Leu Phe Ile Ile Glu
      275      280      285
Gly Met Leu Thr Ala Leu Gly Val Gln Ser Thr Tyr Arg Thr Asn Met
      290      295      300
Val Pro Pro Glu Val Gly Leu Pro Cys Glu Glu Arg Ile Tyr Gln Asp
      305      310      315      320
Gly Leu Ala Pro Pro Pro Pro Thr Ile Ala Gln Phe Asp Asn Arg
      325      330      335
Val Phe Ala Asp Glu Glu Arg Asp Phe Ser Ser Phe Thr Tyr Arg Ile
      340      345      350
Glu Ala Val Arg Ile Leu Gly Arg Val Val Gly Ile Gln Asp Met Val
      355      360      365
Glu Gly Gln Gln Asp His Val Glu Ala Ile Asp Ala Arg Ile Thr Ser
      370      375      380
Trp Phe His His Leu Pro Glu Ser Lys Ala Glu Leu Leu Arg Pro Asp
      385      390      395      400
Gly Ser Val Asp Glu Met Met Phe Gln Ala Thr Met Ile Val Asn Gly
      405      410      415
Ala Ser Ile Tyr Leu His Phe Pro Arg Ser Asp Leu Leu Ser Ser Pro
      420      425      430
Ala Met Ala Ala Glu Val Ile Cys Gly His His Gly Pro Cys Ser Ile
      435      440      445
Pro Ala Phe Ser His His Ala His Ala Met Lys Ala Leu Lys Ala Ala
      450      455      460
Ser Glu Ile Ser Ser Leu Ala Ser Ile Arg Met Pro Val Val Lys His
      465      470      475      480
Thr Pro Phe Phe Ile Cys Ala Leu Val Met Ser Ser Ile Val Gln Leu
      485      490      495
Ala Ala Cys Ser Val Lys Ala Gly Gln Met Pro Asp Pro Ser Arg Asp
      500      505      510
Arg Leu Thr Leu Thr Ile Gly Val Phe Lys Ser Leu Ala Arg Thr Trp
      515      520      525
Ala Ile Ser Gln Thr Ile Met Arg Gln Ile Lys Ala Val Ser Arg Asp
      530      535      540
Val Met Asp Met Gly Leu Arg Pro Ala Met Asp Gln Ile Asp Leu Thr
      545      550      555      560
Thr Leu Leu Asp Ser Gly Arg Phe Leu Met Pro Asp Gly Leu Met Arg
      565      570      575

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<210> 103
 <211> 1272
 <212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 103

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atggccaaac ccaaccagcg ccatgcctgt gaccgctgtc acgggtcaaaa actgcgatgc 60
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agccagtcct tacgttccaa ccgactcaag agacataacg cgccgatata tgatgttcct 180
ttggcgtgtg cgcaactagc aaccagtcg accgacccaa acacacctca atttggtgca 240
tacatgagcc aaccctcctc cgccggcggt gacattgaca tcaacttgct gcagactcaa 300
ttcaccgaca gtactccctg ggctctgccc gccggccgct atccctctcc agcatcacag 360
gaaatggaga cttacaatgt gggtcacact gaggcggacc ttccggccac cgcgactgg 420
atgtggcccc cggtcgccaa tgggtccggt caaacgactc ccccgcaaaa ttggcagcaa 480
gcattcaatc aggaatgggc tatgatggcg tcgcagcacc ctgtcgcaac gatggacacg 540
ccgtctcgga catcgccagt aagcgacgcc gtggacccgc cgaagacggt gtgccttctt 600
gcgaccatcc gcgagttgtc agagcttaac gtcgacctgt acgcacacga agcgacggtc 660
cccagacctc ctgcatctct ggaggaaccg atcagctgga agaacaagga tttcgccatc 720
gatcggactt tccacctgtc ccagcggctc attgagatcg tcaacaaaacg atatccgcgc 780
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<210> 104

<211> 424

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 104

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Met Ala Lys Pro Asn Gln Arg His Ala Cys Asp Arg Cys His Gly Gln
 1          5          10          15
Lys Leu Arg Cys Ile His Ser Gly Gly Gly Pro Cys Val Arg Cys Ala
 20          25          30
Lys Ala Lys Ala Thr Cys Ser Trp Ser Gln Ser Leu Arg Ser Asn Arg
 35          40          45
Leu Lys Arg His Asn Ala Pro Ile Ser Asp Val Pro Leu Ala Cys Ala
 50          55          60
Gln Leu Ala Thr Gln Ser Thr Asp Pro Asn Thr Pro Gln Phe Gly Ala
 65          70          75          80
Tyr Met Ser Gln Pro Ser Ser Ala Gly Val Asp Ile Asp Ile Asn Leu
 85          90          95
Leu Gln Thr Gln Phe Thr Asp Ser Thr Pro Trp Ala Leu Pro Ala Gly
100          105          110
Arg Tyr Pro Ser Pro Ala Ser Gln Glu Met Glu Thr Tyr Asn Val Gly
115          120          125
His Thr Glu Ala Asp Leu Pro Ala Thr Ala Asp Trp Met Trp Pro Ala
130          135          140
Val Ala Asn Gly Pro Val Gln Thr Thr Pro Pro Ala Asn Trp Gln Gln

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145          150          155          160
Ala Phe Asn Gln Glu Trp Ala Met Met Ala Ser Gln His Pro Val Ala
          165          170          175
Thr Met Asp Thr Pro Ser Arg Thr Ser Pro Val Ser Asp Ala Val Asp
          180          185          190
Pro Pro Lys Thr Val Cys Leu Leu Ala Thr Ile Arg Glu Leu Ser Glu
          195          200          205
Leu Asn Val Asp Leu Tyr Ala His Glu Ala Thr Val Pro Arg Pro Pro
          210          215          220
Ala Ser Leu Glu Glu Pro Ile Ser Trp Lys Asn Lys Asp Phe Ala Ile
225          230          235          240
Asp Arg Thr Phe His Leu Ser Gln Arg Leu Ile Glu Ile Val Asn Lys
          245          250          255
Arg Tyr Pro Arg Tyr Leu Glu Thr Ala Arg Met Gln Thr Pro Glu Gly
          260          265          270
Thr Pro Glu Arg Thr Ser Glu Ser Ser Leu Ser Gly Pro Pro Leu Asp
          275          280          285
Gln Gly Ser Cys Leu Leu Val Leu Ser Cys Tyr Thr Arg Leu Ile Glu
          290          295          300
Thr Tyr Asp Arg Ile Phe Ala Asn Met Gln Gly Cys Leu Asp Arg Ser
305          310          315          320
Ser Val Thr Ala Arg Glu Asp Tyr Val Asn Met Pro Ser Val Gln Val
          325          330          335
Gly Ser Phe Ser Leu Pro His Ser Ser Ser Leu Gln Ile Val Leu Ile
          340          345          350
Leu Gln Leu Ala Arg Gln Leu Leu Thr Arg Met Gly Glu Ile Ile Lys
          355          360          365
Ala Val Gln Pro Glu Lys Arg Thr Asn Pro Ala Asp Val Thr Leu Ser
          370          375          380
Glu Ser Ala Thr Gly Gly Leu Leu Leu Ser Ser Ala Leu Glu Thr Val
385          390          395          400
Ser Ala Glu Glu Asp Arg Leu Met Lys Arg Ile Thr Lys Leu Arg Ser
          405          410          415
Thr Leu Ile Glu Leu Asn Ile Leu
          420

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<210> 105

<211> 1473

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 105

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atccgttccg gttcggctct tgtatgggat gagcgagaag cgggtatgcg gcgatggacc 180
gatgggaagt catggagcgc cagccgtgtg tctggtagct ttttgacgta tcgtgaaatg 240
gaaggcaagc gtggaggtgg tagcgtctct cagggttctg cgtcccaggg aggtaaaacg 300
cctgagagtc ggggcagtga cgatgatcgt gcgatggaa cagatgaggg accagatggg 360
taccgttaca aaccagatgg cttgatgaag cagtctttca gtatcacaac ctccaacggt 420
caacatctgc atctcattag ctactattca cgatctcacc cttcggccgc caacttaca 480
caaccaacta cggatcctgc gctacgccat gttcgcccc agaaaggcct ctatcccag 540
tcaacagtca acgatcagca aaacctccct gtcgttacc gtggacctat gcaaggcgct 600
gcgtacccca taactcccca tcctctcggc gcataccgc gcgtcactca tacacagcca 660

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caatacggcc ctggctcctt ttatctgccc ccggtagggt ccaatggaca tcctcattat 780
ggcccgccac atcatcagcc tccacctcat caacatggcg gtggactacc accccctcca 840
cacgggatga caagcccgta tgatcgacca cctcacaatg aatcaacatt gcctccagct 900
ggaccaccgt cacaacagcc aagctacatg aaccgggtcac cgcgctcaat acacgaccat 960
gctcaagccc acgcccattg tcacgctcac gctcaagctc aggctcaagc tcaagctcag 1020
gctcaagctc aagctcaggc acaggcccat gccacgagc aacgcacccc gcctgtctac 1080
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cagccaaatg gccacgcgca cagccctcat ctggcggaagc aggagcatcc cgccgcgctg 1200
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<210> 106

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 106

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          20           25           30
Leu Ser Glu Lys Glu Arg Gln Ser Ile Arg Ser Gly Ser Val Phe Val
          35           40           45
Trp Asp Glu Arg Glu Ala Gly Met Arg Arg Trp Thr Asp Gly Lys Ser
          50           55           60
Trp Ser Ala Ser Arg Val Ser Gly Ser Phe Leu Thr Tyr Arg Glu Met
          65           70           75           80
Glu Gly Lys Arg Gly Gly Gly Ser Val Ser Gln Gly Ser Ala Ser Arg
          85           90           95
Gly Gly Lys Thr Pro Glu Ser Arg Gly Ser Asp Asp Asp Arg Ala Asp
          100          105          110
Gly Thr Asp Glu Gly Pro Asp Gly Tyr Arg Tyr Lys Pro Asp Gly Leu
          115          120          125
Met Lys Gln Ser Phe Ser Ile Thr Thr Ser Asn Gly Gln His Leu His
          130          135          140
Leu Ile Ser Tyr Tyr Ser Arg Ser His Pro Ser Ala Ala Asn Leu Gln
          145          150          155          160
Gln Pro Thr Thr Asp Pro Ala Leu Arg His Val Arg Pro Gln Lys Gly
          165          170          175
Leu Tyr Pro Glu Ser Thr Val Asn Asp Gln Gln Asn Leu Pro Val Val
          180          185          190
Thr Arg Gly Pro Met Gln Gly Ala Ala Tyr Pro Ile Thr Pro His Pro
          195          200          205
Leu Gly Ala Tyr Pro Arg Val Thr His Thr Gln Pro Tyr Pro Pro Ala
          210          215          220
Tyr Ala Trp Pro Pro Thr Pro Leu Ala Thr Pro Pro Thr Val Ser Val
          225          230          235          240
Gln Tyr Gly Pro Gly Pro Ser Tyr Leu Pro Pro Val Gly Ala Asn Gly
          245          250          255
His Pro His Tyr Gly Pro Pro His His Gln Pro Pro Pro His Gln His

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<210> 107
<211> 2577
<212> DNA
<213> Artificial Sequence
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<220>
<223> fungal gene

<400> 107

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gtgcgccaag ccgacattct attctcatac caggtcgggt tgccgggcat gatccgaggt 1260
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accattgtta ctctcgacct ataccacggc ctgtcattgc aggtcagcgg ccggccatca 1860
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ctgagcagcg gaatgagccc gatgaacccg ggccagccgc cgtttgctga tcccatgttc 2160
aagatgggag attcgccgat gggaactgga acaggtgctg tgggcgcctc ggccgaaatg 2220
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<210> 108

<211> 859

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 108

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Asn Ser Ser Ser Ala Gly His Ser Pro Asp Tyr Arg Val Val Arg Lys
      20             25             30
Arg Asn Arg Val Pro Leu Ser Cys Gly Pro Cys Arg His Arg Lys Leu
      35             40             45
Lys Cys Asn Arg Thr His Pro Cys Glu Asn Cys Val Lys Arg Gly Asp
      50             55             60
Ala Ala Ser Cys Asn Tyr Ala Gln Pro Asn Ser Arg Lys Lys Asn Pro
65             70             75             80
Gln Gln Ser Ser Thr Thr Pro Asp Asp Met Gln Asn Arg Ile Asp Arg
      85             90             95
Leu Glu Gly Leu Val Leu Ser Leu Met Thr Asn Gly Ser Gln Ser Ala
      100            105            110
Gly Pro Asn Ala Ala Met Ala Ala Ile Ser Gly Glu Ser Ser Ala Gly
      115            120            125
Ser Thr Arg Phe Ser His Asp Leu Asp Ala Glu Glu Glu Gly Met Glu
130            135            140
Gly Ala Glu Glu Ser Asp Thr Asp Gln Val Thr Lys Ser Phe Gly Ile
145            150            155            160
Met Lys Met Asp Asn Asn Lys Ser Tyr Tyr Ile Ser Asp Ala His Trp

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Thr Trp Gly Arg Glu Arg Arg Asp Glu Met Thr Ala Ala Ile Gln His
 625 630 635 640
 Ser Lys Glu Ile Trp Asp Glu Ser Arg Asp Glu Ser Met Glu Ala Trp
 645 650 655
 Lys Ala Ser Thr Val Leu Gly Val Met Leu Ser Lys Leu His Met Thr
 660 665 670
 Val Pro Gly Leu Glu Asn Ser Ala Gly Ala Ala Ser Phe Glu Pro Gln
 675 680 685
 Asp Glu Lys Gln Asn Ala Ala Met Thr Leu Gly Leu Leu Ser Ser Gly
 690 695 700
 Met Ser Pro Met Asn Pro Gly Gln Pro Pro Phe Ala Asp Pro Met Phe
 705 710 715 720
 Lys Met Gly Asp Ser Pro Met Gly Thr Gly Thr Gly Ala Val Gly Ala
 725 730 735
 Ser Ala Glu Met Pro Gly Ala Leu Ser Pro Phe Ser Ser Met Phe Gly
 740 745 750
 Gln Met Pro Asp Met Gln Val Asn Leu Asp Trp Asp Ala Trp Asp Thr
 755 760 765
 Tyr Ile Gln Asn Pro Thr Leu Asp Thr Thr Asn Gln Phe Trp Pro Met
 770 775 780
 Met Asp Ala Gln Arg Gln Ala Thr Pro Gln Ser Gly Gly Met Ser Gln
 785 790 795 800
 Pro Ser Val Ser Ser Pro Leu Ala Ser Gly Arg Val Pro Ser Ile Ser
 805 810 815
 Gly Val Pro Arg Ile Pro Thr Met Tyr Ser Ala Ser Ser Asn Ser Pro
 820 825 830
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<210> 109

<211> 3732

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 109

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<210> 110

<211> 1244

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 110

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			20					25					30		
Val	Ala	Gln	Ala	Leu	His	Ala	Gln	Gly	Thr	Tyr	Thr	Gly	Trp	Arg	Ala
		35					40					45			
Glu	Val	Pro	Met	Lys	Glu	Arg	Val	Val	Arg	Val	Tyr	Gln	Met	Phe	Thr
	50					55					60				
Ser	Leu	Arg	Leu	Ile	Gln	Pro	Gln	Ala	Asp	Leu	Gln	His	Leu	Ala	Gln
65					70				75						80
Ala	Ala	Leu	Ser	Phe	Glu	Gln	Lys	Ala	Phe	Lys	Asp	Ala	Gln	Gln	Lys
				85					90					95	
Val	Asp	Tyr	Asp	Lys	Glu	Cys	Asn	Asp	Lys	Leu	Leu	His	Ile	Arg	Asp
			100					105					110		
Thr	Arg	Ala	Arg	Gln	Ala	Ala	Val	Met	Gln	Asn	Gly	Met	Ile	Pro	Pro
		115					120					125			
Gly	Ala	Pro	Lys	Ala	Gly	Gly	Met	Arg	Gly	Val	Gly	Gln	Pro	Ser	Phe
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Pro	Gln	Gln	Met	Asn	Arg	Ala	Met	Gln	Ser	Asn	Pro	Met	Ala	Gly	Gln
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Gln	Ala	Met	Ala	Met	Gly	Met	Thr	Asp	Pro	Asn	Gln	Gln	Ala	Ala	Met
				165					170					175	
Pro	Gln	Arg	Ser	Gln	Gln	Gln	Gln	Ala	Met	Met	Gln	Gln	Gln	Gln	Gln
			180					185					190		
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Arg	Ala
		195					200					205			
Gln	Gln	Arg	Ser	Ala	Asn	Thr	Leu	Ala	Leu	Val	Asp	Glu	Leu	Asn	Asn
	210					215					220				
Leu	Thr	Pro	Gln	Glu	Tyr	Glu	Asn	Val	Asn	Arg	Val	Ala	His	Gln	Ile
225					230					235					240
Met	Thr	Lys	Thr	Ser	Pro	Val	Asp	Ala	Glu	Lys	Ile	Lys	Arg	Asn	Leu
				245					250					255	
Gln	Asn	Met	Asn	Pro	Val	Gln	Arg	Arg	Tyr	Leu	Thr	Glu	Arg	Asn	Ile
			260					265					270		
Asp	Pro	Val	Ala	Tyr	Phe	Phe	Arg	Ser	Gln	Ala	Leu	Ala	His	Leu	Lys
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Arg	Gln	Met	Lys	Ala	Arg	Val	Asp	Met	Ser	His	Pro	Gln	Asn	Thr	Gly
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Val	Asp	Pro	Asn	Asn	Val	Met	Met	Gly	Ala	Asp	Pro	Thr	Met	Asn	Pro
305					310					315					320
Gln	Met	Phe	Pro	Asn	Met	Met	Asn	Leu	Gln	Arg	Asn	Ser	Ala	Phe	Ala
				325					330					335	
Met	Gly	Asn	Gln	Pro	Asn	Met	Asp	Pro	Ser	Ser	Phe	Ile	Gly	Asn	Val
			340					345					350		
Glu	Asn	Ile	Gln	Gly	Gln	Gln	Ala	Asp	Gly	Leu	Arg	Ser	Gln	Glu	Ala
		355					360					365			
Gly	Gln	Leu	Val	Val	Pro	Ala	Ser	Ser	Ser	Gln	Met	Asn	Gln	Gln	Pro
	370					375					380				
Phe	Asn	Asn	Ala	Gln	Asn	Thr	Phe	Pro	Met	Gly	Gln	Gln	Leu	Ala	Gln
385					390					395					400
Gly	Gly	Gln	Ala	Asn	Leu	Gly	Ala	Ala	Gly	Ile	Asn	Pro	Gln	Met	Phe
				405					410					415	
Ala	Gln	Gln	His	Met	Gln	Asn	Thr	Pro	Asn	Met	Pro	Pro	Asp	Arg	Pro
			420					425					430		
Gln	Pro	Ala	Ala	Pro	Phe	Gln	Pro	Gln	Thr	Gln	Ala	Gln	Asn	Gln	Ala
		435					440					445			
Gln	Ala	Gln	Ala	Arg	Ala	Gln	Ala	Ala	Gln	Lys	Ala	Gln	Met	Ala	Ile

450		455		460
Ser Gln Ala Gly Gln	Ala Asn Ser His Leu Gln Gln Pro Met Pro Gln			
465	470	475	480	
Gln Ser Pro Ala Met	Pro Met Leu Asn Arg Pro Met Pro Pro Gly Gln			
	485	490	495	
Met Ser Pro Ala Gln	Met Ala Ala Gln Val Arg Pro Pro Ser Arg Ala			
	500	505	510	
Pro Ala Met Gly Gln	Gln Pro Ser Met Gly Gly Gln Gln Pro Met Gln			
	515	520	525	
Gly Arg Pro Gln Ile	Pro Pro Gly Leu Pro Pro Ala Ile Gln Glu Gln			
	530	535	540	
Leu Ala Gln Met Ser	Pro Glu Gln Leu Asn Arg Val Leu Ala Gln Arg			
545	550	555	560	
Arg Ala Met Ala Asn	Asn Pro Ala Leu Ala Arg Ala Asn Ala Ala Arg			
	565	570	575	
Gln Ser Val Pro Met	Gln Gln Ser Val Ser Gln Ser Ala Gln Ala Gln			
	580	585	590	
Ser Met Ala Asn Asn	Gln Asn Met Arg Ala Met Asn Val Gln Ala Gln			
	595	600	605	
Leu Ala Gly Met Gly	Gly Ala Gln Gln Met Met Pro Gly Gln Gln Met			
	610	615	620	
Ser Leu Gln Gln Gln	Gln Gln Gln Gln Gln Gln Gln Arg Gln Glu			
625	630	635	640	
Leu Tyr Lys Met Gln	Leu Leu Gln Gln Ser Gly Gly Asn Leu Glu Leu			
	645	650	655	
Ser Asn Glu Gln Ser	Lys Glu Met Asp Arg Leu His Phe Pro Pro Ser			
	660	665	670	
Leu Leu Gly Asn Asn	Pro Asn Ile Val Ser Leu Val Pro Lys Asn Ile			
	675	680	685	
Lys Thr Trp Gly Gln	Leu Lys Gln Trp Ala Ala Thr Asn Pro Gln Leu			
	690	695	700	
Pro Gly Gly Leu Asn	Leu Gln Lys Leu Met Ala Leu Gln Lys Phe His			
705	710	715	720	
Phe Thr Gln Ile Leu	Asn Gln Ser Lys Glu Arg Ser Arg Asn Pro Asp			
	725	730	735	
Gln Ala Gly Gln Gly	Pro Trp Met Ser Gly Pro Thr Gln Ala Pro Gln			
	740	745	750	
Gln Pro Pro Met Met	Asn Pro Gln Gln Phe Pro Pro Gly Gln Gln Gln			
	755	760	765	
Ala Ala Ile Asn Met	Ala Ala Ile Arg Pro Val Thr Ala Gln Asp Ile			
	770	775	780	
Gln Ala Ala Arg Gln	Arg His Pro Ala Met Ala Gln Asn Phe Thr Asp			
785	790	795	800	
Asp Gln Ile Arg Glu	Ser Leu Asn Lys Ala Arg Gln Arg Gln Leu Met			
	805	810	815	
Leu Leu Ala Gln Gln	Arg Ala Ala Gln Ala Gln Glu Leu Ala Ala Gln			
	820	825	830	
Gln Gln Gln Thr Gln	Ala Leu Gln Gln Thr Pro Val Gly Gly Pro Ala			
	835	840	845	
Pro Gly Pro His Leu	Arg Pro Glu Gly Pro Gly Gln Pro Ala Thr Gln			
	850	855	860	
Pro Gln Gln Gln Ser	Pro Ala Thr Lys Ala Pro Ser Thr Val Pro Gly			
865	870	875	880	
Lys Lys Ala Pro Pro	Ala Lys Gln Gln Pro Ala Lys Arg Lys Leu Pro			
	885	890	895	
Ser Asp Glu Thr Ala	Asp Ala Gln Asn Pro Asp Asn Gln Val Ala Gln			
	900	905	910	

Lys Pro Thr Gln Ala Gly Ala Pro Gln Gly Val Ala Ala Pro Ala Pro
 915 920 925
 Ser Lys Pro Asn Met Pro Phe Thr Arg Glu Gln Leu Ala Ala Met Thr
 930 935 940
 Pro Gln Gln Arg Ala Gln Ile Glu Ala His Met Arg Arg Gln Gln Gly
 945 950 955 960
 Gln Thr Arg Thr Lys Ala Ala Ala Glu Glu Ala Trp Asn Asn Leu Pro
 965 970 975
 Glu Lys Ile Arg Gln Ala Tyr His Asp Thr Leu Lys Gln Ala Pro Pro
 980 985 990
 Met Lys Phe Ala Ala Ile Thr Pro Glu Gln His Ala Ala Met Asn Gln
 995 1000 1005
 Gln Leu Arg Asp Cys Thr Asp Met Leu Gly Arg Met Asp Thr Leu Val
 1010 1015 1020
 Gln Trp Phe Ala Lys Ile Pro Gly Gln Glu Lys Asn Val Arg Ser Leu
 1025 1030 1035 1040
 Leu Ala Met Arg Ile Gln Leu Met Arg Gln Phe Lys Asn Ser Pro Asp
 1045 1050 1055
 Trp Val Leu Asn Asp Ser Leu Thr Ile Ser Pro Glu Asn Leu Thr Ala
 1060 1065 1070
 Thr Ile Asn Tyr Ile Lys Lys Leu Phe His Ala Met Ile Thr Arg Val
 1075 1080 1085
 Ser Gln His Gln Asn Gln Ala Pro Gly Gln Arg Pro Gly Gly Pro Gln
 1090 1095 1100
 Pro Pro Leu Thr Gln Ala Ser Gln Asn Ala Met Pro Ala Leu Asn Ala
 1105 1110 1115 1120
 Thr Asn Leu Gln Gln Leu Gln Gln Glu Glu Ala Leu Gln Arg Ala
 1125 1130 1135
 Arg Arg Ala Ser Ser Gln Thr Ala Val Ser Ala Thr Ser Ala Val Pro
 1140 1145 1150
 Pro Ala Pro Phe Gly Ala Pro Ser Pro Gln Gly Val Pro His Ala Tyr
 1155 1160 1165
 Gly Pro Gly Ser Met Pro Pro Glu Gln Leu Lys Leu Pro Pro Pro Lys
 1170 1175 1180
 Lys Arg Lys Gln Ser His Pro Gly Ala Thr Pro Thr Val Gly Thr Pro
 1185 1190 1195 1200
 Ala Thr Lys Pro Pro Thr Thr Arg Pro Ala Asp Val Lys Met Pro Ala
 1205 1210 1215
 Ala Ala Ser Ser His Val Ile Ser Tyr Val Thr Leu Thr Phe Thr Pro
 1220 1225 1230
 Ser Ser His Ile Arg Ser Asn Arg Lys Gly Arg Ser
 1235 1240

<210> 111

<211> 1302

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 111

atgcaaagcc cccagcagcc acccgacttt ctactgtacc cgactcagtc cacgcgtggg 60
 agcaaaatga tcgccttgga ttctgtccgc cagcagcaga cccattctt ccagaatttc 120
 accatggatc ctgcattcac ggaccctttc gcattccagg tggacacctt cgctagcttc 180
 ggacagcccc ccagttcctc tcgaggcccc cagacttcat attatgatac ccctccgctc 240

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tacacggatt cttactccga ctccaataag accgcccctg ggtttccttc catgccgggt 300
acgcccccca cgcttccctc caccagccg ctggactccc acgttccggg cctgaccgcc 360
ccgtcgggtc cgtctgtcgc cagcgctcc tcctcgcca ttgggtcgcc gtactccggc 420
acggcccatg ccaaccagga gaactgggtc gatacgaacc acggcctggg ccttcccgcc 480
gcggtgatgg gggatctgtt tccgaacgac tacacgggga cgaccctgga ccccgattac 540
tttgccaata aaggcgcgga cagctttgtt gacccttctt tgatcccgct tcagcagcag 600
tcgaatctgt cgaccccggc catctcctac ccggaacaga ctgattatag cctgggtccc 660
ggcggattct tccctcagtc ccctgacct tcccaattcc aatttgcgga cccctatggg 720
ccattcacac agcagccatg ccccatgccc gcctcatccc catctctgat gccctcccat 780
gtcccgcgcc gtctgtctct cctctacgac cgtcggtoct cgggtctctc cgtgcagtc 840
cgtcgtctgc agctgagccc ggcggccagc aacgccgaga tcgaggagga cgccaaggaa 900
aagggccgat gccctcatcc ggattgcggg cgagtcttcc gggacctgaa agcgcacatg 960
ctgacgcata agtcggagcg tccggagaaa tgccccattg tcacttgcca gtaccacacc 1020
aagggggttg cccgcaagta cgacaagaac cgccacacc tgaccacta caagggaacg 1080
atggtttgcg gcttctgccc gggatccggg tcgcccggcg agaagagctt caaccgggcg 1140
gatgtgttca aacgtcatct gacctctgtg cacggtgtgg aacagacccc tcccaactgc 1200
cggaagagaa gccccgcggc cgctcagat catgtaatta gttatgtcac gcttacattc 1260
acgcccctct cccacatccg ctctaaccga aaaggaagga gt 1302

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<210> 112

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 112

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Met Gln Ser Pro Gln Gln Pro Pro Asp Phe Leu Leu Tyr Pro Thr Gln
1      5      10      15
Ser Thr Arg Gly Ser Lys Met Ile Ala Leu Asp Ser Ser Arg Gln Gln
20     25     30
Gln Thr Pro Phe Phe Gln Asn Phe Thr Met Asp Pro Ala Phe Thr Asp
35     40     45
Pro Phe Ala Phe Gln Val Asp Thr Phe Ala Ser Phe Gly Gln Pro Ala
50     55     60
Ser Ser Ser Arg Gly Pro Gln Thr Ser Tyr Tyr Asp Thr Pro Pro Leu
65     70     75     80
Tyr Thr Asp Ser Tyr Ser Asp Ser Asn Lys Thr Ala Pro Gly Phe Pro
85     90     95
Ser Met Pro Gly Thr Pro Pro Thr Leu Pro Ser Thr Gln Pro Leu Asp
100    105    110
Ser His Val Pro Gly Leu Thr Ala Pro Ser Gly Pro Ser Val Ala Ser
115    120    125
Ala Ser Ser Ser Ala Ile Gly Ser Pro Tyr Ser Gly Thr Ala His Ala
130    135    140
Asn Gln Glu Asn Trp Val Asp Thr Asn His Gly Leu Gly Leu Pro Ala
145    150    155    160
Ala Val Met Gly Asp Leu Phe Pro Asn Asp Tyr Thr Gly Thr Thr Leu
165    170    175
Asp Pro Asp Tyr Phe Ala Asn Lys Gly Ala Asp Ser Phe Val Asp Pro
180    185    190
Ser Leu Ile Pro Leu Gln Gln Gln Ser Asn Leu Ser Thr Pro Ala Ile
195    200    205
Ser Tyr Pro Glu Gln Thr Asp Tyr Ser Leu Val Pro Gly Gly Phe Phe
210    215    220
Pro Gln Ser Pro Asp Pro Ser Gln Phe Gln Phe Ala Asp Pro Tyr Gly

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225					230					235					240
Pro	Phe	Thr	Gln	Gln	Pro	Cys	Pro	Met	Pro	Ala	Ser	Ser	Pro	Ser	Leu
				245					250					255	
Met	Pro	Ser	His	Val	Pro	Pro	Arg	Arg	Leu	Ser	Leu	Tyr	Asp	Arg	Arg
			260					265					270		
Ser	Ser	Val	Ser	Ser	Val	Gln	Ser	Arg	Arg	Ser	Gln	Leu	Ser	Pro	Ala
		275					280					285			
Ala	Ser	Asn	Ala	Glu	Ile	Glu	Glu	Asp	Ala	Lys	Glu	Lys	Gly	Arg	Cys
	290					295					300				
Pro	His	Pro	Asp	Cys	Gly	Arg	Val	Phe	Arg	Asp	Leu	Lys	Ala	His	Met
305					310					315					320
Leu	Thr	His	Gln	Ser	Glu	Arg	Pro	Glu	Lys	Cys	Pro	Ile	Val	Thr	Cys
			325						330					335	
Glu	Tyr	His	Thr	Lys	Gly	Phe	Ala	Arg	Lys	Tyr	Asp	Lys	Asn	Arg	His
			340					345					350		
Thr	Leu	Thr	His	Tyr	Lys	Gly	Thr	Met	Val	Cys	Gly	Phe	Cys	Pro	Gly
		355					360				365				
Ser	Gly	Ser	Pro	Ala	Glu	Lys	Ser	Phe	Asn	Arg	Ala	Asp	Val	Phe	Lys
	370					375					380				
Arg	His	Leu	Thr	Ser	Val	His	Gly	Val	Glu	Gln	Thr	Pro	Pro	Asn	Cys
385					390					395					400
Arg	Lys	Arg	Ser	Pro	Ala	Ala	Ala	Ser	Ser	His	Val	Ile	Ser	Tyr	Val
			405						410					415	
Thr	Leu	Thr	Phe	Thr	Pro	Ser	Ser	His	Ile	Arg	Ser	Asn	Arg	Lys	Gly
			420					425					430		
Arg	Ser														

<210> 113

<211> 1071

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 113

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gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttctttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgcgcgcgcc gccgcgctt 240
tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc gggttcaggac tttaccgtct tcctagaaag cgtcgggtctc 360
tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420
ctacccatgg actcgaaacc ccagcccgt gagagttcca ggctgggcat cgatacaagt 480
ttgtacaaaa aagcaggctc cacaatgacg gagaaccaca ccccttctac tacgcagccg 540
acgttgccctg cgctgtttgc tgaagccgcg ccgatccaag caaaccgcgc tccttctgcc 600
tcagtcacgg cgactgctgc cgcgcgtact gcggcgggtga acaacgcccc ctctatgaac 660
ggcgccggtg agcagttgcc ttgccagtgg gttggttgca cggagaagtc cccactgcc 720
gagtcctctat atgagcatgt ttgcgagcgt catgtttgac gtaaaagcac caacaacctc 780
aacctgacct gccagtgggg cacttgcaac accacaacag tcaagcgtga tcatatcacc 840
tccacatcc gcgttcattg gccacttaag ccgcacaaat gcgacttttg tggtaaggct 900
ttcaagcgcc ccaggattt gaagaagcat gtcaagactc atgcggacga ctccgagatc 960
cgctcccccg aaccgggcat gaagcaccct gatatgatgt tcccccaaaa ccctaagggt 1020
tacgtgctg ccacacatta cttcgaaagc cctatcaacg gcataaatgg g 1071

```


<210> 114
 <211> 1035
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 114
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 gttcagggtc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
 gatttgaacc ttcttttctca tgccgcgagt catgtcgcgc ttgagggaca acaagaaagt 180
 ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
 tctcatatac cagaaagagg gatcactgat aactatgggtg ttgagccttc gattctagac 300
 cttacagatt taggtgatcc gggtcaggac tttaccgtct tcctagaaag cgtcgggtctc 360
 tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420
 ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat gacggagaac 480
 cacacccctt ctactacgca gccgacgttg cctgcgcctg ttgctgaagc cgcgccgatc 540
 caagcaaacc cggtcccttc tgcctcagtc acggcgactg ctgccgccgc tactgcggcg 600
 gtgaacaacg cccctctat gaacggcgcc ggtgagcagt tgccttgcca gtgggttggt 660
 tgcacggaga agtccccac tgccgagtct ctatatgagc atgtttgcga gcgtcatgtt 720
 ggacgtaaaa gcaccaacaa cctcaacctg acctgccagt ggggcacttg caacaccaca 780
 acagtcaagc gtgatcatat cacctcccac atccgcgttc atgtgccact taagccgcac 840
 aaatgcgact tttgtggtaa ggctttcaag cgccccagg atttgaagaa gcatgtcaag 900
 actcatgcgg acgactccga gatccgctcc cccgaaccgg gcatgaagca ccctgatatg 960
 atgttcccc aaaaccctaa gggttacgct gctgccacac attacttcga aagccctatc 1020
 aacggcatca atggg 1035

<210> 115
 <211> 357
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 115
 Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1 5 10 15
 Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
 20 25 30
 His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
 35 40 45
 Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
 50 55 60
 Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Pro Leu
 65 70 75 80
 Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
 85 90 95
 Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
 100 105 110
 Val Phe Leu Glu Ser Val Gly Leu Ser Ser Asp Trp Asp Ser Gly Ile
 115 120 125
 Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
 130 135 140
 Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Ile Asp Thr Ser
 145 150 155 160

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Leu Tyr Lys Lys Ala Gly Ser Thr Met Thr Glu Asn His Thr Pro Ser
      165      170      175
Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu Ala Ala Pro Ile
      180      185      190
Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala Thr Ala Ala Ala
      195      200      205
Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn Gly Ala Gly Glu
      210      215      220
Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys Ser Pro Thr Ala
225      230      235      240
Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser
      245      250      255
Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr Cys Asn Thr Thr
      260      265      270
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
      275      280      285
Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro
      290      295      300
Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Ser Glu Ile
305      310      315      320
Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met Met Phe Pro Gln
      325      330      335
Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe Glu Ser Pro Ile
      340      345      350
Asn Gly Ile Asn Gly
      355

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<210> 116

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 116

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Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1      5      10      15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Ile Val Glu Thr Ala
      20      25      30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
      35      40      45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
      50      55      60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Pro Leu
65      70      75      80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
      85      90      95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
      100      105      110
Val Phe Leu Glu Ser Val Gly Leu Ser Ser Asp Trp Asp Ser Gly Ile
      115      120      125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
      130      135      140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Met Thr Glu Asn
145      150      155      160

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His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu
                165                170                175
Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala
                180                185                190
Thr Ala Ala Ala Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn
                195                200                205
Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys
                210                215                220
Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val
225                230                235                240
Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr
                245                250                255
Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg
                260                265                270
Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala
                275                280                285
Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp
                290                295                300
Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met
305                310                315                320
Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe
                325                330                335
Glu Ser Pro Ile Asn Gly Ile Asn Gly
                340                345

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<210> 117

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 117

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atgaccgccc ccattaccga cgtcagcctg ggggacgagc tccacttaga cggcgaggac 60
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gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcgatacaa gtttgtacaa aaaagcaggc tccacaatgg atcctagaaa ccatccctct 300
cggcctccgt ctaccagtct gcctcaagga tcggcgccctc ttcttctgc tcccatctcg 360
agcatgccaa tgccctcagta cacgatgcag cctcagtacc cagtctctca gccgcacacc 420
ctgcctcctc tgcaacccca tcatagccag tcgcccgcctc ctactcgtat catggggcag 480
ccgccgtacc ggcctgatct gaacaggtac ccgcgatcaa gtcacgatgt ttacgcgtct 540
tctgctgcgc cgataatgcc ccacactacc gtgggcagct tgccctccgac atctttcctt 600
tctcatccca atccgcaggc gcaggcacag gcgcagcaat cgcgcacta tcctcctcct 660
catagcgtgc tccgccccgc ttccagcgct cagtctgtacc cgcagccaat tgcgccggcg 720
cctccccggg accgctcgtgc tgacttcaac aatggacttc cttcaggagc attcagttat 780
tcggacggaa agcctcaagg ttgggacccc gttgctgcga atggtgctgc gccgatatcc 840
gggaaggact cccccgaac ccaggttgtt ggttctcagg ggcgacgcgg tatccttccg 900
agtgttccgg gacgcgcaac tccggtcaca aatggtgtta acggcaccgg caagaacact 960
actatccgg ccaaggatgc cgatggaaag ttcccttgcc cgaactgtaa caagacttat 1020
cttcatgcc aagcatctcaa gcgccatctg ctacgccaca ctggtgaccg cccgtacatg 1080
tgtgttcttt gaaaagacac cttctctcgc agtgatatcc tgaaacgtca tttccaaaaa 1140
tgctcaatca ggcgtggtaa cccacccgga gcaacgcact tgtcgcaccc caatgcgcat 1200
gtgaagaggt cccaacagca ggctgcggcg aatcctgtaa aacctgtcca ggatgaagtc 1260
agtagtaccg tcccgccctc caatggcatc ccgggcacga cttacggcga gggagccgctc 1320

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aacggcaatg gactagctcc ggcccggcca ggttacgcgg atcaccagac tatgggcttc 1380
ccaatgtcat ccgtcaacgg gatgggcccgt ggtcagccgt aagacgcgtt tcccggcggc 1440
cggccgcata aaggagcccc ttggccacaa gctcccaagc agagcccgtg tctcgtgcag 1500
ccgggtgctg acccttctgg ccaccagttg aatattgacc gaaacatcga gcaggtaaaa 1560
caaccggttg ttcaagaccc caagcgccct gtgatgccag gacatcccgg ccaccccggg 1620
gagcttgact ggacgtctat gttccaacct caagctcccg agggctacat gttctccag 1680
tctatgcctg gtggtaaga gcccatccac gctcatgtcg agaccgagcg aaagtattac 1740
cccaccacta ccgctggtca agagagtggg atgaacggtc tctatctggc ttcgactatg 1800
agtggcgacg gcaccgttca gcccgccaga caa 1833

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<210> 118

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 118

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gtggcgatgg cgcataccga cgcgctagac gatttcgatc tggacatgtt gggggacggg 120
gattccccgg gtccgggatt tacccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgcctcgg gcattgacga ctttggggga 240
atcatggatc ctagaaacca tccctctcgg cctccgtcta ccagtctgcc tcaaggatcg 300
gcgcctcttc cttctgctcc catctcgagc atgccaatgc ctacgtacac gatgcagcct 360
cagtaccagc tctctcagcc gcacaccctg cctcctctgc aaccccatca tagccagtcg 420
cccgtccttc actcgtacat ggggcagccg ccgtaccggc ctgatctgaa caggtacccc 480
gcatcaagtc acgatgttta cgcgtcttct gctgcgccga taatgcccc aactaccgtg 540
ggcagcttgc ctccgacatc tttcctttct catcccaatc cgcaggcgca ggcacaggcg 600
cagcaatcgc cgcactatcc tctcctcat agcgtgctcc cgcccgttc cagcgctcag 660
tcgtaccgcg agccaattgc gccggcgcc ccccgggacc gtcgtgctga cttcaacaat 720
ggacttcctt caggagcatt cagttattcg gacggaaagc ctcaagggtg ggaccccggt 780
gctgcgaatg gtgctgcgcc gtatcccggg aaggactccc ccgaacca ggttggttgt 840
tctcaggggc gacgcggtat ccttcaggat gttccgggac gcgcaactcc ggtcacaaat 900
ggtgttaacg gcaccggcaa gaacactact atcccgcca aggatgccga tggaaagtgc 960
ccttgcccga actgtaacaa gacttatctt catgccagc atctcaagc ccatctgcta 1020
cgccacactg gtgaccgccc gtacatgtgt gttctttgca aagacacctt ctctcgagc 1080
gatatcctga aacgtcattt ccaaaaatgc tcaatcaggc gtggttaacc caccggagca 1140
acgcacttgt cgacccccaa tgcgcatgtg aagaggtccc aacagcaggc tgcggcgaat 1200
cctgtaaaac ctgtccagga tgaagtcagt agtaccgtcc cgctcccaa tggcatcccg 1260
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tacgcgatc accagactat gggcttccca atgcatccg tcaacgggat gggccgttgt 1380
cagcctgaag acggttttcc cggcgccgg cgcatcaag gagccccttg gccacaagct 1440
cccaagcaga gccgtatctc cgtgcagccg ggtgctgacc cttctggcca ccagttgaat 1500
attgaccgaa acatcgagca ggtaaaacaa ccggttggtc aagaccccaa gcgccctgtg 1560
atgccaggac atcccgccca ccccggtgag cttgactgga cgtctatgtt ccaacctcaa 1620
gtccccgagg gctacatgtt ctcccagctc atgcctggtg gtcaagagcc catccacgct 1680
catgtcgaga ccgagcgaaa gtattacccc accactaccg ctggtcaaga gagtggaaatg 1740
aacggtctct atctggcttc gactatgagt ggcgacggca ccgttcagcc cgccagacaa 1800

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<210> 119

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 119

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1          5          10          15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
          20          25          30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
          35          40          45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
          50          55          60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
65          70          75          80
Ile Asp Thr Ser Leu Tyr Lys Lys Ala Gly Ser Thr Met Asp Pro Arg
          85          90          95
Asn His Pro Ser Arg Pro Pro Ser Thr Ser Leu Pro Gln Gly Ser Ala
          100          105          110
Pro Leu Pro Ser Ala Pro Ile Ser Ser Met Pro Met Pro Gln Tyr Thr
          115          120          125
Met Gln Pro Gln Tyr Pro Val Ser Gln Pro His Thr Leu Pro Pro Leu
130          135          140
Gln Pro His His Ser Gln Ser Pro Ala Pro His Ser Tyr Met Gly Gln
145          150          155          160
Pro Pro Tyr Arg Pro Asp Leu Asn Arg Tyr Pro Ala Ser Ser His Asp
          165          170          175
Val Tyr Ala Ser Ser Ala Ala Pro Ile Met Pro His Thr Thr Val Gly
          180          185          190
Ser Leu Pro Pro Thr Ser Phe Leu Ser His Pro Asn Pro Gln Ala Gln
          195          200          205
Ala Gln Ala Gln Gln Ser Pro His Tyr Pro Pro Pro His Ser Val Leu
210          215          220
Pro Pro Ala Ser Ser Ala Gln Ser Tyr Pro Gln Pro Ile Ala Pro Ala
225          230          235          240
Pro Pro Arg Asp Arg Arg Ala Asp Phe Asn Asn Gly Leu Pro Ser Gly
          245          250          255
Ala Phe Ser Tyr Ser Asp Gly Lys Pro Gln Gly Trp Asp Pro Val Ala
          260          265          270
Ala Asn Gly Ala Ala Pro Tyr Pro Gly Lys Asp Ser Pro Arg Thr Gln
          275          280          285
Val Val Gly Ser Gln Gly Arg Gly Ile Leu Pro Ser Val Pro Gly
          290          295          300
Arg Ala Thr Pro Val Thr Asn Gly Val Asn Gly Thr Gly Lys Asn Thr
305          310          315          320
Thr Ile Pro Ala Lys Asp Ala Asp Gly Lys Phe Pro Cys Pro Asn Cys
          325          330          335
Asn Lys Thr Tyr Leu His Ala Lys His Leu Lys Arg His Leu Leu Arg
          340          345          350
His Thr Gly Asp Arg Pro Tyr Met Cys Val Leu Cys Lys Asp Thr Phe
          355          360          365
Ser Arg Ser Asp Ile Leu Lys Arg His Phe Gln Lys Cys Ser Ile Arg
          370          375          380
Arg Gly Asn Pro Thr Gly Ala Thr His Leu Ser His Pro Asn Ala His
385          390          395          400
Val Lys Arg Ser Gln Gln Gln Ala Ala Ala Asn Pro Val Lys Pro Val
          405          410          415
Gln Asp Glu Val Ser Ser Thr Val Pro Pro Pro Asn Gly Ile Pro Gly
          420          425          430

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Thr Thr Tyr Gly Glu Gly Ala Val Asn Gly Asn Gly Leu Ala Pro Ala
  435          440          445
Arg Pro Gly Tyr Ala Asp His Gln Thr Met Gly Phe Pro Met Ser Ser
  450          455          460
Val Asn Gly Met Gly Arg Gly Gln Pro Glu Asp Ala Phe Pro Gly Gly
  465          470          475          480
Arg Pro His Gln Gly Ala Pro Trp Pro Gln Ala Pro Lys Gln Ser Pro
          485          490          495
Tyr Leu Val Gln Pro Gly Ala Asp Pro Ser Gly His Gln Leu Asn Ile
  500          505          510
Asp Arg Asn Ile Glu Gln Val Lys Gln Pro Val Val Gln Asp Pro Lys
  515          520          525
Arg Pro Val Met Pro Gly His Pro Gly His Pro Gly Glu Leu Asp Trp
  530          535          540
Thr Ser Met Phe Gln Pro Gln Ala Pro Glu Gly Tyr Met Phe Ser Gln
  545          550          555          560
Ser Met Pro Gly Gly Gln Glu Pro Ile His Ala His Val Glu Thr Glu
          565          570          575
Arg Lys Tyr Tyr Pro Thr Thr Thr Ala Gly Gln Glu Ser Gly Met Asn
  580          585          590
Gly Leu Tyr Leu Ala Ser Thr Met Ser Gly Asp Gly Thr Val Gln Pro
  595          600          605
Ala Arg Gln
  610

```

<210> 120

<211> 600

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 120

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
  1          5          10          15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
  20          25          30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
  35          40          45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
  50          55          60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
  65          70          75          80
Ile Met Asp Pro Arg Asn His Pro Ser Arg Pro Pro Ser Thr Ser Leu
          85          90          95
Pro Gln Gly Ser Ala Pro Leu Pro Ser Ala Pro Ile Ser Ser Met Pro
  100          105          110
Met Pro Gln Tyr Thr Met Gln Pro Gln Tyr Pro Val Ser Gln Pro His
  115          120          125
Thr Leu Pro Pro Leu Gln Pro His His Ser Gln Ser Pro Ala Pro His
  130          135          140
Ser Tyr Met Gly Gln Pro Pro Tyr Arg Pro Asp Leu Asn Arg Tyr Pro
  145          150          155          160
Ala Ser Ser His Asp Val Tyr Ala Ser Ser Ala Ala Pro Ile Met Pro
          165          170          175

```

```

His Thr Thr Val Gly Ser Leu Pro Pro Thr Ser Phe Leu Ser His Pro
180 185 190
Asn Pro Gln Ala Gln Ala Gln Ala Gln Ser Pro His Tyr Pro Pro
195 200 205
Pro His Ser Val Leu Pro Pro Ala Ser Ser Ala Gln Ser Tyr Pro Gln
210 215 220
Pro Ile Ala Pro Ala Pro Pro Arg Asp Arg Arg Ala Asp Phe Asn Asn
225 230 235 240
Gly Leu Pro Ser Gly Ala Phe Ser Tyr Ser Asp Gly Lys Pro Gln Gly
245 250 255
Trp Asp Pro Val Ala Ala Asn Gly Ala Ala Pro Tyr Pro Gly Lys Asp
260 265 270
Ser Pro Arg Thr Gln Val Val Gly Ser Gln Gly Arg Arg Gly Ile Leu
275 280 285
Pro Ser Val Pro Gly Arg Ala Thr Pro Val Thr Asn Gly Val Asn Gly
290 295 300
Thr Gly Lys Asn Thr Thr Ile Pro Ala Lys Asp Ala Asp Gly Lys Phe
305 310 315 320
Pro Cys Pro Asn Cys Asn Lys Thr Tyr Leu His Ala Lys His Leu Lys
325 330 335
Arg His Leu Leu Arg His Thr Gly Asp Arg Pro Tyr Met Cys Val Leu
340 345 350
Cys Lys Asp Thr Phe Ser Arg Ser Asp Ile Leu Lys Arg His Phe Gln
355 360 365
Lys Cys Ser Ile Arg Arg Gly Asn Pro Thr Gly Ala Thr His Leu Ser
370 375 380
His Pro Asn Ala His Val Lys Arg Ser Gln Gln Gln Ala Ala Ala Asn
385 390 395 400
Pro Val Lys Pro Val Gln Asp Glu Val Ser Ser Thr Val Pro Pro Pro
405 410 415
Asn Gly Ile Pro Gly Thr Thr Tyr Gly Glu Gly Ala Val Asn Gly Asn
420 425 430
Gly Leu Ala Pro Ala Arg Pro Gly Tyr Ala Asp His Gln Thr Met Gly
435 440 445
Phe Pro Met Ser Ser Val Asn Gly Met Gly Arg Gly Gln Pro Glu Asp
450 455 460
Ala Phe Pro Gly Gly Arg Pro His Gln Gly Ala Pro Trp Pro Gln Ala
465 470 475 480
Pro Lys Gln Ser Pro Tyr Leu Val Gln Pro Gly Ala Asp Pro Ser Gly
485 490 495
His Gln Leu Asn Ile Asp Arg Asn Ile Glu Gln Val Lys Gln Pro Val
500 505 510
Val Gln Asp Pro Lys Arg Pro Val Met Pro Gly His Pro Gly His Pro
515 520 525
Gly Glu Leu Asp Trp Thr Ser Met Phe Gln Pro Gln Ala Pro Glu Gly
530 535 540
Tyr Met Phe Ser Gln Ser Met Pro Gly Gly Gln Glu Pro Ile His Ala
545 550 555 560
His Val Glu Thr Glu Arg Lys Tyr Tyr Pro Thr Thr Thr Ala Gly Gln
565 570 575
Glu Ser Gly Met Asn Gly Leu Tyr Leu Ala Ser Thr Met Ser Gly Asp
580 585 590
Gly Thr Val Gln Pro Ala Arg Gln
595 600

```

<210> 121

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 121

```

atgaccgccc ccattaccga cgtcagcctg ggggacgagc tccacttaga cggcgaggac 60
gtggcgatgg cgcgatgccga cgcgctagac gatttcgatac tggacatgtt gggggacggg 120
gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcgatacaa gtttgtacaa aaaagcaggc tccacaatgg ttcttctcaa aaagcatttg 300
aaagatgtca accgtgagga tcagaggcaa atgccgaggc aacggctgcc atctattcaa 360
gaaatatttg gggagacttt tctggcgatt ccttcaaatc catcatatgc actgccttct 420
cacaccgac atgccgctcc accggctttg ccgctgtgt atgaaattgc ccattcaatc 480
gaaggggctc cgtcaaatga gcaaggttta ttacccaaaa tttcaacagt ggagagatct 540
ttgggcatta tctctcccg caatgagctc cagcatccgg aggtaatag cccggaaaat 600
ccatccttct ctccgaacgg ttgttctctt aacgaaagcc gtcgcttttc aaagcaccgc 660
gacctatcta tacctcaacc gggtttattg tcatgcatc ccattggatt agcacagccg 720
tcctttgtcg aacctccaaa tgtgtttcat ggatttccca tcaggaaaat accaaactcg 780
ataccgcctc agccaaagca gttatgtctg ccgaaaaaac gaacaccgag ttctcttgat 840
ttcagctctg tttttaaggt gatcgagaca gtcagcgcac agaccttggc ttcgtgagg 900
tatcactccg caatgagtca gtcagacaac catcaaagat ccctccctgg actatctatc 960
actgagataa atggcctcct cagtcaggag cagcaaaagc aggatgtctt gatttatatt 1020
agggatgaac ttgtgcgctt cgaccaatac caagccttag cgcagcagaa tactcgggca 1080
gccgcatgta tggcgggtgg ggctgaccga ggtctttgt catcagtcac taaacagagc 1140
aagacccata aagtctctaa acaaaaaaga gaatggcacg gggatagtgc tcttcgttgt 1200
catagctgca accgttctga aacaccagaa tggcgctcgt gtcgggacgg ccccggaact 1260
ctttgtaacg cctgtggttt acattatgca aaattgtctc gacgaacggg caaatttgtg 1320
gcgttgagcg atattggcat caggggcaaaa aca 1353

```

<210> 122

<211> 1320

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 122

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atgaccgccc ccattaccga cgtcagcctg ggggacgagc tccacttaga cggcgaggac 60
gtggcgatgg cgcgatgccga cgcgctagac gatttcgatac tggacatgtt gggggacggg 120
gattccccgg gtccgggatt tccccccac gactccgccc cctacggcgc tctggatatg 180
gccgacttcg agtttgagca gatgtttacc gatgccctgg gcattgacga ctttggggga 240
atcatggttc ttctcaaaaa gcatttgaaa gatgtcaacc gtgaggatca gaggcaaatg 300
ccgaggcaac ggctgccatc tattcaagaa atatttgagg agacttttct ggcgattcct 360
tcaaatccat catatgcaat gccttctcac accagacatg ccgctccacc ggccttgccg 420
gctgtgtatg aaattgcccc ttcaatcgaa ggggctccgt caaatgagca aggtttatta 480
cccaaaattt caacagtggg gagatctttg gccattatct ctcccgtaaa tgagctccag 540
catccggagg taatacgccc ggaaaatcca tccttctctc cgaacggttg ttctcttaac 600
gaaagccgtc gcttttcaaa gcacccggac ctatctatac ctcaaccggg tttattgtca 660
tgcgatccca tggatttagc acagccgtcc tttgtcgaa ctccaaatgt gtttcatgga 720
tttcccatca ggaaaatacc aaactcgata ccgcctcagc caaagcagtt atgtctgccg 780
gaaaaacgaa caccgagttc tcttgatttc agtctgtttt ttaagggtgat cgagacagtc 840
agcgcacaga ccttggtctt cgtgcggtat cactccgcaa tgagtcagtc agacaaccat 900
caaagatccc tccctggact atctatcact gagataaatg gcctcctcag tcaggagcag 960

```



```

caaaagcagg atgtcttgat ttatattagg gatgaacttg tgcgcttcga ccaataccaa 1020
gccttagcgc agcagaatac tcgggcagcc gcatgtatgg cgggtggggc tgaccgaggt 1080
ctttgttcat cagtcactaa acagagcaag acccataaag tctctaaaca aaaaagagaa 1140
tggcacgggg atagtgtctt tcgttgtcat agctgcaacc gttctgaaac accagaatgg 1200
cgtcgtggtc cggacggccc ccgaactctt tgtaacgcct gtggtttaca ttatgcaaaa 1260
ttgtctcgac gaacggggcaa atttgtggcg ttggacgata ttggcatcag gggcaaaa 1320

```

<210> 123

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 123

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1           5           10           15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
      20           25           30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
      35           40           45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
      50           55           60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
      65           70           75           80
Ile Asp Thr Ser Leu Tyr Lys Lys Ala Gly Ser Thr Met Val Leu Leu
      85           90           95
Lys Lys His Leu Lys Asp Val Asn Arg Glu Asp Gln Arg Gln Met Pro
      100          105          110
Arg Gln Arg Leu Pro Ser Ile Gln Glu Ile Phe Gly Glu Thr Phe Leu
      115          120          125
Ala Ile Pro Ser Asn Pro Ser Tyr Ala Leu Pro Ser His Thr Arg His
      130          135          140
Ala Ala Pro Pro Ala Leu Pro Ala Val Tyr Glu Ile Ala His Ser Ile
      145          150          155          160
Glu Gly Ala Pro Ser Asn Glu Gln Gly Leu Leu Pro Lys Ile Ser Thr
      165          170          175
Val Glu Arg Ser Leu Gly Ile Ile Ser Pro Val Asn Glu Leu Gln His
      180          185          190
Pro Glu Val Ile Arg Pro Glu Asn Pro Ser Phe Ser Pro Asn Gly Cys
      195          200          205
Ser Leu Asn Glu Ser Arg Arg Phe Ser Lys His Pro Asp Leu Ser Ile
      210          215          220
Pro Gln Pro Gly Leu Leu Ser Cys Asp Pro Met Asp Leu Ala Gln Pro
      225          230          235          240
Ser Phe Val Glu Pro Pro Asn Val Phe His Gly Phe Pro Ile Arg Lys
      245          250          255
Ile Pro Asn Ser Ile Pro Pro Gln Pro Lys Gln Leu Cys Leu Pro Glu
      260          265          270
Lys Arg Thr Pro Ser Ser Leu Asp Phe Ser Leu Phe Phe Lys Val Ile
      275          280          285
Glu Thr Val Ser Ala Gln Thr Leu Ala Phe Val Arg Tyr His Ser Ala
      290          295          300
Met Ser Gln Ser Asp Asn His Gln Arg Ser Leu Pro Gly Leu Ser Ile
      305          310          315          320

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```

Thr Glu Ile Asn Gly Leu Leu Ser Gln Glu Gln Gln Lys Gln Asp Val
      325      330      335
Leu Ile Tyr Ile Arg Asp Glu Leu Val Arg Phe Asp Gln Tyr Gln Ala
      340      345      350
Leu Ala Gln Gln Asn Thr Arg Ala Ala Ala Cys Met Ala Gly Gly Ala
      355      360      365
Asp Arg Gly Leu Cys Ser Ser Val Thr Lys Gln Ser Lys Thr His Lys
      370      375      380
Val Ser Lys Gln Lys Arg Glu Trp His Gly Asp Ser Ala Leu Arg Cys
      385      390      395      400
His Ser Cys Asn Arg Ser Glu Thr Pro Glu Trp Arg Arg Gly Pro Asp
      405      410      415
Gly Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu His Tyr Ala Lys Leu
      420      425      430
Ser Arg Arg Thr Gly Lys Phe Val Ala Leu Asp Asp Ile Gly Ile Arg
      435      440      445
Gly Lys Thr
      450

```

<210> 124

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 124

```

Met Thr Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1      5      10      15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
      20      25      30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
      35      40      45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
      50      55      60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
      65      70      75      80
Ile Met Val Leu Leu Lys Lys His Leu Lys Asp Val Asn Arg Glu Asp
      85      90      95
Gln Arg Gln Met Pro Arg Gln Arg Leu Pro Ser Ile Gln Glu Ile Phe
      100      105      110
Gly Glu Thr Phe Leu Ala Ile Pro Ser Asn Pro Ser Tyr Ala Leu Pro
      115      120      125
Ser His Thr Arg His Ala Ala Pro Pro Ala Leu Pro Ala Val Tyr Glu
      130      135      140
Ile Ala His Ser Ile Glu Gly Ala Pro Ser Asn Glu Gln Gly Leu Leu
      145      150      155      160
Pro Lys Ile Ser Thr Val Glu Arg Ser Leu Gly Ile Ile Ser Pro Val
      165      170      175
Asn Glu Leu Gln His Pro Glu Val Ile Arg Pro Glu Asn Pro Ser Phe
      180      185      190
Ser Pro Asn Gly Cys Ser Leu Asn Glu Ser Arg Arg Phe Ser Lys His
      195      200      205
Pro Asp Leu Ser Ile Pro Gln Pro Gly Leu Leu Ser Cys Asp Pro Met
      210      215      220

```

Asp Leu Ala Gln Pro Ser Phe Val Glu Pro Pro Asn Val Phe His Gly
 225 230 235 240
 Phe Pro Ile Arg Lys Ile Pro Asn Ser Ile Pro Pro Gln Pro Lys Gln
 245 250 255
 Leu Cys Leu Pro Glu Lys Arg Thr Pro Ser Ser Leu Asp Phe Ser Leu
 260 265 270
 Phe Phe Lys Val Ile Glu Thr Val Ser Ala Gln Thr Leu Ala Phe Val
 275 280 285
 Arg Tyr His Ser Ala Met Ser Gln Ser Asp Asn His Gln Arg Ser Leu
 290 295 300
 Pro Gly Leu Ser Ile Thr Glu Ile Asn Gly Leu Ser Gln Glu Gln
 305 310 315 320
 Gln Lys Gln Asp Val Leu Ile Tyr Ile Arg Asp Glu Leu Val Arg Phe
 325 330 335
 Asp Gln Tyr Gln Ala Leu Ala Gln Gln Asn Thr Arg Ala Ala Ala Cys
 340 345 350
 Met Ala Gly Gly Ala Asp Arg Gly Leu Cys Ser Ser Val Thr Lys Gln
 355 360 365
 Ser Lys Thr His Lys Val Ser Lys Gln Lys Arg Glu Trp His Gly Asp
 370 375 380
 Ser Ala Leu Arg Cys His Ser Cys Asn Arg Ser Glu Thr Pro Glu Trp
 385 390 395 400
 Arg Arg Gly Pro Asp Gly Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu
 405 410 415
 His Tyr Ala Lys Leu Ser Arg Arg Thr Gly Lys Phe Val Ala Leu Asp
 420 425 430
 Asp Ile Gly Ile Arg Gly Lys Thr
 435 440

<210> 125

<211> 1071

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 125

atgctcgagt tagtcgatgc tattccgctt cagaccacgc cagtctctcc tgctcctgaa 60
 gttcagggtc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
 gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
 ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
 tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
 cttacagatt taggtgatcc gggttcaggac tttaccgtct tcctagaaag cgtctgtctc 360
 tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccactagc 420
 ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat cgatacaagt 480
 ttgtacaaaa aagcaggctc cacaatgacg gagaaccaca ccccttctac tacgcagccg 540
 acgttgctcgc cgctgtttgc tgaagccgcg ccgatccaag caaaccgggc tccttctgcc 600
 tcagtcacgg cgactgctgc cgccgtact gcggcgggtga acaacgcccc ctctatgaac 660
 ggcgccggtg agcagttgcc ttgccagtgg gttggttgca cggagaagtc cccactgcc 720
 gagtctctat atgagcatgt ttgcgagcgt catgttggaac gtaaaagcac caacaacctc 780
 aacctgacct gccagtgggg cacttgcaac accacaacag tcaagcgtga tcatatcacc 840
 tcccacatcc gcgttcatgt gccacttaag ccgcacaaat gcgacttttg tggttaaggct 900
 ttcaagcgcc cccaggattt gaagaagcat gtcaagactc atgcggacga ctccgagatc 960
 cgctcccccg aaccgggcat gaagcaccct gatatgatgt tccccaaaa ccctaagggt 1020
 tacgctgctg ccacacatta cttcgaaagc cctatcaacg gcatcaatgg g 1071

<210> 126
 <211> 1035
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 126
 atgctcgagt tagtcgatgc tattccgctt cagacccagc cagttcctcc tgctcctgaa 60
 gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
 gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
 ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
 tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
 cttacagatt taggtgatcc ggttcaggac ttaccgtctc tcctagaaag cgtctgtctc 360
 tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420
 ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat gacggagAAC 480
 cacacccctt ctactacgca gccgacgttg cctgcgcctg ttgctgaagc cgcgccgac 540
 caagcaaacc cggtcctctc tgccctcagtc acggcgactg ctgccgccgc tactgcggcg 600
 gtgaacaacg cccctctat gaacggcgcc ggtgagcagt tgccttgcca gtgggttggt 660
 tgcacggaga agtccccac tgccgagtct ctatatgagc atgtttgcga gcgtcatgtt 720
 ggacgtaaaa gcaccaacaa cctcaacctg acctgccagt ggggcacttg caacaccaca 780
 acagtcaagc gtgatcatat cacctcccac atccgcgttc atgtgccact taagccgcac 840
 aaatgcgact tttgtggtaa ggctttcaag cgccccagg atttgaagaa gcatgtcaag 900
 actcatgcgg acgactccga gatccgctcc cccgaaccgg gcatgaagca ccctgatatg 960
 atgttcccc aaacccctaa gggttacgct gctgccacac attacttcga aagccctatc 1020
 aacggcatca atggg 1035

<210> 127
 <211> 357
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 127
 Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1 5 10 15
 Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
 20 25 30
 His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
 35 40 45
 Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
 50 55 60
 Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Leu
 65 70 75 80
 Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
 85 90 95
 Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
 100 105 110
 Val Phe Leu Glu Ser Val Cys Leu Ser Ser Asp Trp Asp Ser Gly Ile
 115 120 125
 Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
 130 135 140
 Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Ile Asp Thr Ser

```

145          150          155          160
Leu Tyr Lys Lys Ala Gly Ser Thr Met Thr Glu Asn His Thr Pro Ser
          165          170          175
Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu Ala Ala Pro Ile
          180          185          190
Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala Thr Ala Ala Ala
          195          200          205
Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn Gly Ala Gly Glu
          210          215          220
Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys Ser Pro Thr Ala
225          230          235          240
Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser
          245          250          255
Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr Cys Asn Thr Thr
          260          265          270
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
          275          280          285
Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro
          290          295          300
Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Ser Glu Ile
305          310          315          320
Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met Met Phe Pro Gln
          325          330          335
Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe Glu Ser Pro Ile
          340          345          350
Asn Gly Ile Asn Gly
          355

```

<210> 128

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 128

```

Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
1          5          10          15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
          20          25          30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
          35          40          45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
          50          55          60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Leu
65          70          75          80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
          85          90          95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
          100          105          110
Val Phe Leu Glu Ser Val Cys Leu Ser Ser Asp Trp Asp Ser Gly Ile
          115          120          125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
130          135          140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Met Thr Glu Asn

```

145		150		155		160
His Thr Pro Ser Thr	Thr Gln Pro Thr	Leu Pro Ala Pro Val	Ala Glu			
	165	170	175			
Ala Ala Pro Ile Gln	Ala Asn Pro Ala	Pro Ser Ala Ser	Val Thr Ala			
	180	185	190			
Thr Ala Ala Ala Thr	Ala Ala Val Asn	Asn Ala Pro Ser	Met Asn			
	195	200	205			
Gly Ala Gly Glu Gln	Leu Pro Cys Gln	Trp Val Gly Cys	Thr Glu Lys			
	210	215	220			
Ser Pro Thr Ala Glu	Ser Leu Tyr Glu	His Val Cys Glu	Arg His Val			
	225	230	235			240
Gly Arg Lys Ser Thr	Asn Asn Leu Asn	Leu Thr Cys Gln	Trp Gly Thr			
	245	250	255			
Cys Asn Thr Thr Thr	Val Lys Arg Asp	His Ile Thr Ser	His Ile Arg			
	260	265	270			
Val His Val Pro Leu	Lys Pro His Lys	Cys Asp Phe Cys	Gly Lys Ala			
	275	280	285			
Phe Lys Arg Pro Gln	Asp Leu Lys Lys	His Val Lys Thr	His Ala Asp			
	290	295	300			
Asp Ser Glu Ile Arg	Ser Pro Glu Pro	Gly Met Lys His	Pro Asp Met			
	305	310	315			320
Met Phe Pro Gln Asn	Pro Lys Gly Tyr	Ala Ala Ala Thr	His Tyr Phe			
	325	330	335			
Glu Ser Pro Ile Asn	Gly Ile Asn Gly					
	340	345				

<210> 129

<211> 1071

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 129

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gttcagggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgccgcc gccgccgctt 240
tctcatatac cagaaagagg gatcactgat aactatgggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc ggttcaggac tttaccgtct tcctagaaag cgtcgatctc 360
tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaaactagc 420
ctacccatgg actcgaaacc cccagcccgt gagagttcca ggctgggcat cgatacaagt 480
ttgtacaaaa aagcaggctc cacaatgacg gagaaccaca ccccttctac tacgcagccg 540
acgttgccctg cgctgtttgc tgaagccgcg ccgatccaag caaaccoggc tccttctgcc 600
tcagtcacgg cgactgctgc cgccgctact gcggcggtga acaacgcccc ctctatgaac 660
ggcgccgggtg agcagttgcc ttgccagtgg gttggttgca cggagaagtc cccactgcc 720
gagtccttat atgagcatgt ttgcgagcgt catgttggac gtaaaagcac caacaacctc 780
aacctgacct gccagtgggg cacttgcaac accacaacag tcaagcgtga tcatatcacc 840
tcccacatcc gcgttcatgt gccacttaag ccgcacaaat gcgacttttg tggtaaggct 900
ttcaagcgcc cccaggattt gaagaagcat gtcaagactc atgcggacga ctccgagatc 960
cgctcccccg aaccgggcat gaagcaccct gatatgatgt tccccaaaa ccctaagggt 1020
tacgctgctg ccacacatta cttcgaaagc cctatcaacg gcatcaatgg g 1071

```

<210> 130

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 130

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gttcaggttc agccccctcc aatcgtggag acggcccatt tcaacccttc atggggatat 120
gatttgaacc ttcttttctca tgccgcgagt catgtcgctc ttgagggaca acaagaaagt 180
ctagagactc ttcggaagcc ttcgcaaaac attcaagcgc cgccgcgcgc gccgcgcgtt 240
tctcatatac cagaaagagg gatcactgat aactatggtg ttgagccttc gattctagac 300
cttacagatt taggtgatcc ggttcaggac tttaccgtct tcctagaaag cgtcgatctc 360
tcttcggact gggactccgg catcttctct agtgtagaag agcccttatt gccaactagc 420
ctaccatggg actcgaaacc cccagcccgt gagagttcca ggctgggcat gacggagaac 480
cacacccctt ctactacgca gccgacgttg cctgcgcctg ttgctgaagc cgcgcgcgatc 540
caagcaaacc cggtcccttc tgctcagtc acggcgactg ctgccgcgcg tactgcggcg 600
gtgaacaacg cccctctat gaacggcgcc ggtgagcagt tgccttgcca gtgggttggg 660
tgcacggaga agtccccac tgccgagtct ctatatgagc atgtttgcga gcgtcatgtt 720
ggacgtaaaa gcaccaacaa cctcaacctg acctgccagt ggggcacttg caacaccaca 780
acagtcaagc gtgatcatat cacctcccac atccgcgttc atgtgccact taagccgcac 840
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actcatgcgg acgactccga gatccgctcc cccgaaccgg gcatgaagca ccctgatatg 960
atgttcccc aaaaccctaa gggttacgct gctgccacac attacttca aagccctatc 1020
aacggcatca atggg                                     1035

```

<210> 131

<211> 357

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 131

```

Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1             5             10             15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
      20             25             30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
      35             40             45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
      50             55             60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Pro Leu
      65             70             75             80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
      85             90             95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
      100            105            110
Val Phe Leu Glu Ser Val Asp Leu Ser Ser Asp Trp Asp Ser Gly Ile
      115            120            125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
      130            135            140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Ile Asp Thr Ser
      145            150            155            160
Leu Tyr Lys Lys Ala Gly Ser Thr Met Thr Glu Asn His Thr Pro Ser
      165            170            175

```

```

Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu Ala Ala Pro Ile
      180      185      190
Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala Thr Ala Ala Ala
      195      200      205
Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn Gly Ala Gly Glu
      210      215      220
Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys Ser Pro Thr Ala
225      230      235      240
Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser
      245      250      255
Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr Cys Asn Thr Thr
      260      265      270
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
      275      280      285
Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro
      290      295      300
Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Ser Glu Ile
305      310      315      320
Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met Met Phe Pro Gln
      325      330      335
Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe Glu Ser Pro Ile
      340      345      350
Asn Gly Ile Asn Gly
      355

```

<210> 132

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 132

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Met Leu Glu Leu Val Asp Ala Ile Pro Leu Gln Thr Gln Pro Val Pro
 1      5      10      15
Pro Ala Pro Glu Val Gln Val Gln Pro Pro Pro Ile Val Glu Thr Ala
      20      25      30
His Phe Asn Pro Ser Trp Gly Tyr Asp Leu Asn Leu Leu Ser His Ala
      35      40      45
Ala Ser His Val Ala Leu Glu Gly Gln Gln Glu Ser Leu Glu Thr Leu
      50      55      60
Arg Lys Pro Ser Gln Asn Ile Gln Ala Pro Pro Pro Pro Pro Pro Leu
65      70      75      80
Ser His Ile Pro Glu Arg Gly Ile Thr Asp Asn Tyr Gly Val Glu Pro
      85      90      95
Ser Ile Leu Asp Leu Thr Asp Leu Gly Asp Pro Val Gln Asp Phe Thr
      100      105      110
Val Phe Leu Glu Ser Val Asp Leu Ser Ser Asp Trp Asp Ser Gly Ile
      115      120      125
Phe Ser Ser Val Glu Glu Pro Leu Leu Pro Thr Ser Leu Pro Met Asp
      130      135      140
Ser Lys Pro Pro Ala Arg Glu Ser Ser Arg Leu Gly Met Thr Glu Asn
145      150      155      160
His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala Pro Val Ala Glu
      165      170      175

```


Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala Ser Val Thr Ala
 180 185 190
 Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala Pro Ser Met Asn
 195 200 205
 Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly Cys Thr Glu Lys
 210 215 220
 Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys Glu Arg His Val
 225 230 235 240
 Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Thr
 245 250 255
 Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg
 260 265 270
 Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala
 275 280 285
 Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp
 290 295 300
 Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys His Pro Asp Met
 305 310 315 320
 Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala Thr His Tyr Phe
 325 330 335
 Glu Ser Pro Ile Asn Gly Ile Asn Gly
 340 345

<210> 133

<211> 810

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 133

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gctactgcgg cggtgaacaa cgccccctct atgaacggcg ccggtgagca gttgccttgc 180
cagtggggtg gttgcacgga gaagtcccc actgccgagt ctctatatga gcatgtttgc 240
gagcgtcatg ttggacgtaa aagcaccaac aacctcaacc tgacctgcca gtggggcact 300
tgcaacacca caacagtcaa gcgtgatcat atcacctccc acatccgcgt tcatgtgcca 360
cttaagccgc acaaatgcga cttttgtggt aaggctttca agcgccccca ggatttgaag 420
aagcatgtca agactcatgc ggacgactcc gagatccgct cccccgaacc gggcatgaag 480
caccctgata tgatgttccc ccaaaaccct aagggttacg ctgctgccac acattacttc 540
gaaagcccta tcaacggcat caatggggga tctaccgccc ccattaccga cgtcagcctg 600
ggggacgagc tccacttaga cggcgaggac gtggcgatgg cgcgatgccg cgcgctagac 660
gatttcgatac tggacatgtt gggggacggg gattcccccg gtccgggatt tccccccac 720
gactccgccc cctacggcgc tctggatatg gccgacttcg agtttgagca gatgtttacc 780
gatgccctgg gcattgacga ctttggggga

```

<210> 134

<211> 804

<212> DNA

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 134

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gccgcgccga tccaagcaaa cccggctcct tctgcctcag tcacggcgac tgctgccgcc 120
gctactgcgg cggatgaaca cgcctcctct atgaacggcg ccggtgagca gttgccttgc 180
cagtgggttg gttgcacgga gaagtcccc actgccgagt ctctatatga gcatgtttgc 240
gagcgtcatg ttggacgtaa aagcaccaac aacctcaacc tgacctgcca gtggggcact 300
tgcaacacca caacagtcaa gcgtgatcat atcacctccc acatccgcgt tcatgtgcca 360
cttaagccgc acaaatgcga cttttgtggt aaggctttca agcgccccca ggatttgaag 420
aagcatgtca agactcatgc ggacgactcc gagatccgct ccccggaacc gggcatgaag 480
caccctgata tgatgttccc ccaaaaccct aagggttacg ctgctgccac acattacttc 540
gaaagcccta tcaacggcat caatgggacc gccccatta ccgacgtcag cctgggggac 600
gagctccact tagacggcga ggacgtggcg atggcgcatg ccgacgcgct agacgatttc 660
gatctggaca tggtggggga cggggattcc ccgggtccgg gatttacctc ccacgactcc 720
gccccctacg gcgctctgga tatggccgac ttcgagtttg agcagatgtt taccgatgcc 780
ctgggcattg acgacttttg gggg

```

<210> 135

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 135

```

Met Thr Glu Asn His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala
 1          5          10          15
Pro Val Ala Glu Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala
          20          25          30
Ser Val Thr Ala Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala
          35          40          45
Pro Ser Met Asn Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly
          50          55          60
Cys Thr Glu Lys Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys
65          70          75          80
Glu Arg His Val Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys
          85          90          95
Gln Trp Gly Thr Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr
          100          105          110
Ser His Ile Arg Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe
          115          120          125
Cys Gly Lys Ala Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys
          130          135          140
Thr His Ala Asp Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys
145          150          155          160
His Pro Asp Met Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala
          165          170          175
Thr His Tyr Phe Glu Ser Pro Ile Asn Gly Ile Asn Gly Gly Ser Thr
          180          185          190
Ala Pro Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly
          195          200          205
Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu
          210          215          220
Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
225          230          235          240
Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
          245          250          255
Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly

```

260

265

270

<210> 136
 <211> 268
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 136
 Met Thr Glu Asn His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala
 1 5 10 15
 Pro Val Ala Glu Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala
 20 25 30
 Ser Val Thr Ala Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala
 35 40 45
 Pro Ser Met Asn Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly
 50 55 60
 Cys Thr Glu Lys Ser Pro Thr Ala Glu Ser Leu Tyr Glu His Val Cys
 65 70 75 80
 Glu Arg His Val Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys
 85 90 95
 Gln Trp Gly Thr Cys Asn Thr Thr Thr Val Lys Arg Asp His Ile Thr
 100 105 110
 Ser His Ile Arg Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe
 115 120 125
 Cys Gly Lys Ala Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys
 130 135 140
 Thr His Ala Asp Asp Ser Glu Ile Arg Ser Pro Glu Pro Gly Met Lys
 145 150 155 160
 His Pro Asp Met Met Phe Pro Gln Asn Pro Lys Gly Tyr Ala Ala Ala
 165 170 175
 Thr His Tyr Phe Glu Ser Pro Ile Asn Gly Ile Asn Gly Thr Ala Pro
 180 185 190
 Ile Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu Asp
 195 200 205
 Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
 210 215 220
 Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp Ser
 225 230 235 240
 Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln Met
 245 250 255
 Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly Gly
 260 265

<210> 137
 <211> 2415
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fungal gene

<400> 137

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ccatttaacg ctccaaagct atctaataga aagtggccgg ataaccggat caccgagggct 180
cctcgttggt tatcaacaga tttagagagat ggtaaccaat ctctgccgga tcccatgtca 240
gtggaacaaa agaaagaata ctttcacaag ctgggtcaata ttgggttcaa agaaatcgag 300
gtttccttcc cctctgcatc tcaaacagat ttcgacttca ctagatatgc tgtagaaaac 360
gccccagacg atgttagtat tcaatgtctt gtccaatcta gagaacactt gattaagaga 420
acggtggaag cattaacagg tgctaaaaag gctactatac atacttactt ggcaacaagt 480
gatatgttcc gtgaaattgt ttttaatatg tctagagagg aagctatttc caaggcagta 540
gaggccacca aactagttag gaaactaact aaggatgacc cttcccaaca agccactcgt 600
tggtcctatg agttttcccc cgaatgtttc agtgatactc caggtgaatt tgctgtagaa 660
atthgcgaag ctgttaagaa ggcttgaggaa cctaccgagg aaaatccaat cattttcaac 720
ttacctgcta ccgtagaagt tgccctctcca aatgtttatg ctgacagat tgaatacttc 780
gctacccata ttactgagcg tgagaagggt tgcactctca cacattgtca caatgaccgt 840
ggttgcggtg tcgcgcgcac agagttagggt atgcttgacg gtgccgaccg tgtagaagga 900
tgtctctttg gtaatggtga acgtacaggt aatgtggact tggttactgt tgctatgaat 960
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agtttagtca attataatgt tgaaaaattc ggcaactgaac gtagagtgtt cactggtcaa 1500
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atgcccttga gagccttcaa cccagtcagc tccttccggt gggcgccggg catgactatc 1860
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cttgccggtat tcggaatctt gcacgccctc gctcaagcct tcgtcactgg tcccgccacc 2040
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ccgctgatcg tcacggcgat ttatgccgcc tcggcgagca catggaacgg gttggcatgg 2340
attgtaggcg ccgccctata ccttgtctgc ctcccccggt tgcgtcgcgg tgcattggagc 2400
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<210> 138

<211> 805

<212> PRT

<213> Artificial Sequence

<220>

<223> fungal gene

<400> 138

```

Met Val Lys Glu Ser Ile Ile Ala Leu Ala Glu His Ala Ala Ser Arg
 1             5             10             15
Ala Ser Arg Val Ile Pro Pro Val Lys Leu Ala Tyr Lys Asn Met Leu
                20             25             30
Lys Asp Pro Ser Ser Lys Tyr Lys Pro Phe Asn Ala Pro Lys Leu Ser
                35             40             45

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Asn Arg Lys Trp Pro Asp Asn Arg Ile Thr Arg Ala Pro Arg Trp Leu
 50          55          60
Ser Thr Asp Leu Arg Asp Gly Asn Gln Ser Leu Pro Asp Pro Met Ser
65          70          75          80
Val Glu Gln Lys Lys Glu Tyr Phe His Lys Leu Val Asn Ile Gly Phe
          85          90          95
Lys Glu Ile Glu Val Ser Phe Pro Ser Ala Ser Gln Thr Asp Phe Asp
          100          105          110
Phe Thr Arg Tyr Ala Val Glu Asn Ala Pro Asp Asp Val Ser Ile Gln
          115          120          125
Cys Leu Val Gln Ser Arg Glu His Leu Ile Lys Arg Thr Val Glu Ala
130          135          140
Leu Thr Gly Ala Lys Lys Ala Thr Ile His Thr Tyr Leu Ala Thr Ser
145          150          155          160
Asp Met Phe Arg Glu Ile Val Phe Asn Met Ser Arg Glu Glu Ala Ile
          165          170          175
Ser Lys Ala Val Glu Ala Thr Lys Leu Val Arg Lys Leu Thr Lys Asp
          180          185          190
Asp Pro Ser Gln Gln Ala Thr Arg Trp Ser Tyr Glu Phe Ser Pro Glu
          195          200          205
Cys Phe Ser Asp Thr Pro Gly Glu Phe Ala Val Glu Ile Cys Glu Ala
210          215          220
Val Lys Lys Ala Trp Glu Pro Thr Glu Glu Asn Pro Ile Ile Phe Asn
225          230          235          240
Leu Pro Ala Thr Val Glu Val Ala Ser Pro Asn Val Tyr Ala Asp Gln
          245          250          255
Ile Glu Tyr Phe Ala Thr His Ile Thr Glu Arg Glu Lys Val Cys Ile
          260          265          270
Ser Thr His Cys His Asn Asp Arg Gly Cys Gly Val Ala Ala Thr Glu
          275          280          285
Leu Gly Met Leu Ala Gly Ala Asp Arg Val Glu Gly Cys Leu Phe Gly
290          295          300
Asn Gly Glu Arg Thr Gly Asn Val Asp Leu Val Thr Val Ala Met Asn
305          310          315          320
Met Tyr Thr Gln Gly Val Ser Pro Asn Leu Asp Phe Ser Asp Leu Thr
          325          330          335
Ser Val Leu Asp Val Val Glu Arg Cys Asn Lys Ile Pro Val Ser Gln
          340          345          350
Arg Ala Pro Tyr Gly Gly Asp Leu Val Val Cys Ala Phe Ser Gly Ser
          355          360          365
His Gln Asp Ala Ile Lys Lys Gly Phe Asn Leu Gln Asn Lys Lys Arg
370          375          380
Ala Gln Gly Glu Thr Gln Trp Arg Ile Pro Tyr Leu Pro Leu Asp Pro
385          390          395          400
Lys Asp Ile Gly Arg Asp Tyr Glu Ala Val Ile Arg Val Asn Ser Gln
          405          410          415
Ser Gly Lys Gly Gly Ala Ala Trp Val Ile Leu Arg Ser Leu Gly Leu
          420          425          430
Asp Leu Pro Arg Asn Met Gln Ile Glu Phe Ser Ser Ala Val Gln Asp
          435          440          445
His Ala Asp Ser Leu Gly Arg Glu Leu Lys Ser Asp Glu Ile Ser Lys
450          455          460
Leu Phe Lys Glu Ala Tyr Asn Tyr Asn Asp Glu Gln Tyr Gln Ala Ile
465          470          475          480
Ser Leu Val Asn Tyr Asn Val Glu Lys Phe Gly Thr Glu Arg Arg Val
          485          490          495
Phe Thr Gly Gln Val Lys Val Gly Asp Gln Ile Leu Tyr Ala Gly Arg

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